

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 18, 2004, 16:14:01; Search time 1405.95 Seconds
(without alignments)
8816.891 Million cell updates/sec

Title: US-10-681-972-12
Perfect score: 286
Sequence: 1 ggggaattcgatccaaagaaa.....taataagatcgaattccc 286

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
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- 30: em_htg_hum.*
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- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	286	100.0	286	6	AR014689	AR014689 Sequence
2	286	100.0	286	6	AR432389	AR432389 Sequence
3	269.2	94.1	270	6	AR014691	AR014691 Sequence
4	269.2	94.1	270	6	AR432391	AR432391 Sequence
5	216.6	75.7	500	6	AR014686	AR014686 Sequence
6	216.6	75.7	500	6	AR432386	AR432386 Sequence
7	190.8	66.7	308	6	AR014682	AR014682 Sequence
8	190.8	66.7	308	6	AR432382	AR432382 Sequence
9	186.6	65.2	451	8	BNUS9459	U59459 Brassica na
10	186.2	65.1	475	8	RSEFP3	X97319 R.sativus m
11	179.8	62.9	414	6	E31545	E31545 Antibacteri
12	179.8	62.9	414	8	AB012871	AB012871 Wasabia j
13	178.8	62.5	395	8	RSU18557	U18557 Raphanus sa
14	178.8	62.5	414	6	A26875	A26875 R.sativus A
15	178.8	62.5	414	6	A39549	A39549 Sequence 37
16	178.8	62.5	414	6	A63404	A63404 Sequence 19
17	178.8	62.5	414	6	AR050153	AR050153 Sequence
18	178.8	62.5	414	6	AR130272	AR130272 Sequence
19	178.8	62.5	414	6	I23728	I23728 Sequence 48
20	178.8	62.5	414	6	AR207337	AR207337 Sequence
21	178.8	62.5	414	6	AR374914	AR374914 Sequence
22	178.4	62.4	363	8	AF528180	AF528180 Brassica
23	178.2	62.3	416	6	E31546	E31546 Antibacteri
24	177.4	62.0	243	6	BD174927	BD174927 Disease t
25	176.8	61.8	364	8	AY383485	AY383485 Brassica
26	176.6	61.7	403	6	A68845	A68845 Sequence 13
27	176.6	61.7	403	8	ATANTSPEC	X91916 A.thaliana
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29	176.2	61.6	400	6	A68647	A68647 Sequence 15
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31	175.8	61.5	243	6	BD174928	BD174928 Disease t
32	175	61.2	288	6	A39553	A39553 Sequence 41
33	175	61.2	288	6	AR050161	AR050161 Sequence
34	175	61.2	288	6	AR130280	AR130280 Sequence
35	175	61.2	288	6	I23736	I23736 Sequence 58
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37	174.2	60.9	243	6	AX412502	AX412502 Sequence
38	174.2	60.9	243	6	AX507351	AX507351 Sequence
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41	172.2	60.2	285	6	AR014692	AR014692 Sequence
42	172.2	60.2	285	6	AR432392	AR432392 Sequence
43	171	59.8	243	6	AX412406	AX412406 Sequence
44	171	59.8	243	6	AX412601	AX412601 Sequence
45	171	59.8	243	6	AX651878	AX651878 Sequence

ALIGNMENTS

RESULT 1
AR014689
LOCUS AR014689
DEFINITION Sequence 12 from patent US 5773696.
ACCESSION AR014689
VERSION AR014689.1
KEYWORDS GI:3972143
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 286)
AUTHORS Liang,J., Shah,D.Maganlal, Wu,Y.Shun. and Rosenberger,C.Annette.
TITLE Antifungal polypeptide and methods for controlling plant pathogenic fungi
JOURNAL Patent: US 5773696-A 12 30-JUN-1998

AR014689 286 bp DNA linear PAT 05-DEC-1998

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QY	61	TCATTGCTGCTCTTTGTTCTCTTTTGGCTGCTTTGAGCACCACCAATGGTGGATCGAAGT	120		
Db	61	TCATTGCTGCTCTTTGTTCTCTTTTGGCTGCTTTGAGCACCACCAATGGTGGATCGAAGT	120		
QY	121	TGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGAAACAACAATGCATGCAGGA	180		
Db	121	TGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGAAACAACAATGCATGCAGGA	180		
QY	181	ACCAATGCGAAGACCTTGAAAGCGAGACACGGATCTTGCAACTATGTCTTCCCGCTC	240		
Db	181	ACCAATGCGAAGACCTTGAAAGCGAGACACGGATCTTGCAACTATGTCTTCCCGCTC	240		
QY	241	ACAAATGATTTTGTACTTCCCCTGTTTAATAAGGATCCGAATTC	286		
Db	241	ACAAATGATTTTGTACTTCCCCTGTTTAATAAGGATCCGAATTC	286		

RESULT 2

AR432389	AR432389	286 bp	DNA	linear	PAT 18-DEC-2003
LOCUS	Sequence 12 from patent US 6653280.				
DEFINITION	Sequence 12 from patent US 6653280.				
ACCESSION	AR432389				
VERSION	AR432389.1	GI:40194666			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1. (bases 1 to 286)				
TITLE	Liang, J., Shah, D.M., Wu, Y.S. and Rosenberger, C.A.				
JOURNAL	Antifungal polypeptide AlyAFP from <i>Alysiaceae</i> and methods for				
FEATURES	controlling plant pathogenic fungi				
	Patent: US 6653280-A 12 25-NOV-2003;				
	Location/Qualifiers				
	1. 286				

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Query Match	100.0%	Score 286;	DB 6;	Length 286;
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Qy	1	GGGAATTCGGATCCAGAAAGCTAATAGATATGGCTAAGTTTGGCTACCATCATCTCTCTTC	60	
Db	1	GGGAATTCGGATCCAGAAAGCTAATAGATATGGCTAAGTTTGGCTACCATCATCTCTCTTC	60	
Qy	61	TCTTTGCTGCTCTTGTCTCTTTGCTTGTGCTTTGAAGCACCAACCAATGGTGGATGCAAGGT	120	
Db	61	TCTTTGCTGCTCTTGTCTCTTTGCTTGTGCTTTGAAGCACCAACCAATGGTGGATGCAAGGT	120	
Qy	121	TGTGCGAGAGACCAAGTCGGGACATGGTCAGGAGTTTGTGGGAAACAAACAATCATGCGAGGA	180	
Db	121	TGTGCGAGAGACCAAGTCGGGACATGGTCAGGAGTTTGTGGGAAACAAACAATCATGCGAGGA	180	
Qy	181	ACCAATGACAGAAACCTTGAAAGACGACAGAACACGGATCTTGGCACTATGTCTTCCAGCTC	240	
Db	181	ACCAATGACAGAAACCTTGAAAGACGACAGAACACGGATCTTGGCACTATGTCTTCCAGCTC	240	
Qy	241	ACAAATGTATTGTGTACTTCCATGTCTTAATGAAGGATCCGAATTC	286	

241 ACAAATGTAATTTGTTACTTCCCATGTTAAATAGGATCCGAATTCCC 286

RESULT 3

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AR014691
LOCUS       AR014691                270 bp    DNA     linear     PAT 05-DEC-1998
DEFINITION  Sequence 14 from patent US 5773696.
ACCESSION   AR014691
VERSION     AR014691.1  GI:3972145
KEYWORDS    .
SOURCE      Unknown.
            Organism      Unknown.
            Unclassified.
            1 (bases 1 to 270)
AUTHORS     Ljang,J.,,Shah,D.Maganlal., Wu,Y.Shun. and Rosenberger,C.Annette.
TITLE       Antifungal polypeptide and methods for controlling plant pathogenic
            fungi
JOURNAL     Patent: US 5773696-A 14 30-JUN-1998;
FEATURES    Location/Qualifiers
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Qy	9	GGATCCAGAAAGTAATAGATATGGCTAACTTTGGCTACCATCATCTCTCTCTCTTTGCT	68	
Db	1	GGATCCAAATAAGTAAATAGTATGGCTAAGTTGCTACCATCATCTCTCTCTTTGCT	60	
Qy	69	GCCTCTGTTCTCTTTGCTGCTTTGAAGCAACCAACATGTTGGATGCAAGTTTGGCGAG	128	
Db	61	GCCTCTGTTCTCTTTGCTGCTTTGAAGCAACCAACATGTTGGATGCAAGTTTGGCGAG	120	
Qy	129	AGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATGCAGGAACCAATGC	188	
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Qy	189	AGAACCTTTGAAGAGCAGACACGGATCTTGCNACTATCTCTCTCCAGCTCACAATGT	248	
Db	181	AGAACTTTGAAGAGCAGAACCGGATCTTGCNACTATCTCTCTCCAGCTCACAATGT	240	
Qy	249	ATTGTTACTTCCCAAGTTAATAGGATCC	278	
Db	241	ATTGTTACTTCCCAAGTTAATAGGATCC	270	

RESULT 4

AR432391	AR432391	270 bp	DNA	linear	PAT 18-DEC-2003
LOCUS	Sequence 14 from patent US 6653280.				
DEFINITION	AR432391				
ACCESSION	AR432391				
VERSION	AR432391.1	GI:40194668			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 270)				
TITLE	Liang, J., Shah, D. M., Wu, Y. S. and Rosenberger, C. A.				
JOURNAL	Antifungal polypeptide AlyAPP from Alyessum and methods for				
FEATURES	controlling plant pathogenic fungi				
source	Patent: US 6653280-A 14 25-NOV-2003;				
	Location/Qualifiers				
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Best Local Similarity	99.3%;	Pred. No. 1.3e-66;			

ORIGIN

Query Match 94.1%; Score 269.2; DB 6; Length 270;
Best Local Similarity 99.3%; Pred. No. 1.3e-66;

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ACCESSION   AR432386
VERSION     AR432386.1  GI:40194663
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 500)
AUTHORS     Liang,J., Shah,D.M., Wu,Y.S. and Rosenberger,C.A.
TITLE       Antifungal polypeptide AlyAFP from Alyssum and methods for
            controlling plant pathogenic fungi
JOURNAL     Patent: US 6653280-A 9 25-NOV-2003;
FEATURES    Location/Qualifiers
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Best Local Similarity 91.6%; Pred. No. 1.8e-51;
Matches 241; Conservative 0; Mismatches 19; Indels 3; Gaps 1;

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Db	110	TCCTGTTCTCTTTGCTGCTTTGAGACACAGACAAUGTGGAGTCACGGAAAGTTGTGGGA	169
Qy	128	GAGACCAAGTGGACATGTCGAGAGTTTGTGGAAACAACAATGCATGCAGGAACCAATG	187
Db	170	GAGTCCAAGTGGAAACATGGTCAGSCGTGTGTGGGAATAATAACGCATGCAGGAACCAATG	229
Qy	188	CAGAAACCTTTGAAGAGCAGAACACGGATCTTGCACATGTCTTCCCACTGCACAAATG	247
Db	230	CAGAAACCTTGAAGAGCAGAACACGGATCTTGCACATGTCTTCCCACTGCACAAATG	289
Qy	248	TATTGTACTTCCCATGTTAAT	270
Db	290	TATTGTACTTCCCATGTTAAT	312

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Db	50	ATCACAGAAGTAATAGATATGCTAAGTGTCTTCCATCATCTCCCTTCTCTCTGTC	109
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Best Local Similarity 84.3%; Pred. No. 7.2e-41;
Matches 215; Conservative 0; Mismatches 37; Indels 3; Gaps 1;
QY 30 ATGGCTAAAGTTGGCTACCATCTCTCTCTTTGCTGCTCTTCTCTTTGCTGCTCTTCTCTTTGCTGCT 89
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QY 90 TTGAGACACCAACATGCTGATGC---AGTTTGTGGAGAGACCAAGTGGGACATGG 146
Db 61 TTGAGACACCAACATGCTGAGAGAGTGGGAGAGTGGGAGAGTCAAGTGGGACATGG 120
QY 147 TCAGGAGTTTGGGAGACCAACATGATCATGACGAGCAACCAATGAGAACCTTGAAGAGCA 206
Db 121 TCAGGAGTTTGGGAGACCAACATGATCATGAGCAACCAATGAGAACCTTGAAGAGCA 180
QY 207 GAACACGAGTCTTGCAACTATGCTCTTCCAGCTCACAATGATTTGTTACTTCCATCT 266
Db 181 CGACATGATCTTGCAACTATGCTCTTCCATATATCTTCCATATACAGATGATCTGTTACTTCCATCT 240
QY 267 TAATAGGATCGAA 281
Db 241 TAATATTCTACAA 255

RESULT 13
RSU18557
LOCUS
DEFINITION
Raphanus sativus antifungal protein 1 preprotein (Rs-APP1) mRNA,
complete cds.
U18557
ACCESSION
U18557.1 GI:644773
VERSION
KEYWORDS
SOURCE
Raphanus sativus (radish)
Raphanus sativus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Raphanus.
1 (sites)
Terras,F.R.G., Eggermont,K., Kovaleva,V., Raikhel,N.V.,
Osborn,R.W., Kester,A., Rees,S.B., Torrekens,S., Van Leuven,F.,
Vanderleyden,J., Cammue,B.P.A. and Broekaert,W.F.
Small cysteine-rich antifungal proteins from radish: their role in
host defense
Plant Cell 7, 568-573 (1995)
2 (bases 1 to 395)
Terras,F.R.
Direct Submission
Submitted (14-DEC-1994) Franky R. Terras, F.A. Janssens Laboratory
of Genetics, Applied Biological Sciences, W. De Croylan 42,
Heverlee, Belgium, B-3001
COMMENT
On Feb 9, 1995 this sequence version replaced gi:609321.
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/translation="antifungal protein 1 preprotein"
/note="Evidence for antifungal activity: Analysis of two
novel classes of antifungal proteins from radish (Raphanus
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Chem. 267, 15301-15309"
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Db 5 ATTAGTGATCATGGCTAAGTTTGTGCTCCATCATGCACTTCTTTTGTGCTCTTCTCTTTGCTGCTCTTCTCT 64
QY 80 CTTTGTGCTCTTGTGAGCAGCAACATGGTGGATGCA---AGTTTGTGGAGAGACCAAG 136
Db 65 TTTTGTGCTCTTGTGAGCAGCAACATGGTGGAGCAGCAAGTTTGTGCGAAGGCCAAG 124
QY 137 TGGGACATGGTGGAGCAGCAACATGGTGGAGCAGCAAGTTTGTGCGAAGGCCAAG 196
Db 125 TGGGACATGGTGGAGCAGCAACATGGTGGAGCAGCAAGTTTGTGCGAAGGCCAAG 184
QY 197 TGAAGACAGCAACACGAGTCTTGGCACTATGTTTCCAGCTCACAATGATTTGTTA 256
Db 185 TGAGAAAGCAGCAGATGGATCTTGCACATATGTTTCCAGCTCACAAGTGTATCTGCTA 244
QY 257 CTTCCCATGTTAAT 270
Db 245 CTTTCTTGTGTTAAT 258

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R. sativus APP1 gene.
A26875
ACCESSION
A26875.1 GI:1247352
VERSION
KEYWORDS
SOURCE
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Raphanus sativus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Raphanus.
1 (bases 1 to 414)
Broekaert,W.F., Cammue,B.P.A., Terras,F.R.G., Vanderleyden,J.,
Osborn,R.W. and Rees,S.B.
BIOCIDAL PROTEINS
Patent: WO 9305153-A 33 18-MAR-1993;

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Search completed: May 18, 2004, 17:59:03
Job time : 1407.95 secs

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DEFINITION	Sequence 37 from Patent WO9416076.				
ACCESSION	A39549				
VERSION	A39549.1	GI:2295842			
KEYWORDS	.				
SOURCE	unidentified				
ORGANISM	unidentified				
REFERENCE	1 (bases 1 to 414)				
AUTHORS	Dubock,A.C., Powell,K.A. and Rees,S.B.				
TITLE	ANTIMICROBIAL-PROTEIN-PRODUCING ENDOSYMBIOTIC MICROORGANISMS				
JOURNAL	Patent: WO 9416076-A 37 21-JUL-1994;				
	ZENECA LTD (GB)				
COMMENT	Other publication AU 5820494 940815.				
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QY	80	CTTTGTCGCCCTTTGAAGCACCAAACAATGGTGGATGCA---AGSTTGTGCAGAGACCACAAAG	136
Dd	66	TTTTTGCTGCTTTTCCAAGCACCAAACAATGGTGGAAACACAGAAGTTGTGCGAAAGGCCAAC	125
QY	137	TGGGACATGTGTCAGAGCTTTGTGGGACACACATGCATGCAGNACCAATGCAGAACCT	196
Dd	126	TGGGACATGTTGAGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCT	185
QY	197	TGAAGAGCAGAAACCGGATCTTGCAACTATGCTTCCCAGCTCACAAAATGATTTTGTTA	256

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OM nucleic - nucleic search, using sw model

Run on: May 18, 2004, 16:12:26 ; Search time 278.85 Seconds
(without alignments)
4357.126 Million cell updates/sec

Title: US-10-681-972-12
Perfect score: 286
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Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	269.2	94.1	270	2	AAT94582
3	256.8	89.8	481	2	AAT99289
4	216.6	75.7	500	2	AAT94581
5	190.8	66.7	308	2	AAT94577
6	179.8	62.9	414	3	AAZ39123
7	178.8	62.5	414	2	AAQ38650
8	178.8	62.5	414	2	AAQ70128
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12	177.4	62.0	243	6	ABQ82690
13	176.6	61.7	403	2	AAV10632
14	176.2	61.6	400	2	AAV10633
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16	175	61.2	261	2	AAQ38652
17	175	61.2	288	2	AAQ70130
18	174.2	60.9	243	6	ABZ14241
19	174.2	60.9	243	7	ABZ42136
20	172.6	60.3	394	9	ADC51221
21	171	59.8	243	7	ADA68378
22	169.4	59.2	426	9	ADC51223
23	167	58.4	575	3	AAZ99339

24	166	58.0	449	3	AAA53190	Aaa53190	Raphanus
25	155	54.2	1973	3	AAC46924	Aac46924	Arabidops
26	120.8	42.2	1616	2	AAV10646	Aav10646	A. thalia
27	116.2	40.6	606	3	AAZ99326	Aaz99326	DNA encod
28	115.4	40.3	522	3	AAZ99324	Aaz99324	DNA encod
29	115.4	40.3	534	3	AAZ51396	Aaz51396	Portion o
30	115.4	40.3	534	3	AAZ99327	Aaz99327	DNA encod
31	115.4	40.3	534	3	AAZ99325	Aaz99325	DNA encod
32	112.4	39.3	243	9	ADC87758	Adc87758	DNA encod
33	111.6	39.0	306	2	AAT94580	Aat94580	Cloned 3'
34	111.6	39.0	437	3	AAZ99331	Aaz99331	DNA encod
35	110	38.5	443	3	AAZ99330	Aaz99330	DNA encod
36	109	38.1	485	3	AAZ99337	Aaz99337	DNA encod
37	108.6	38.0	485	3	AAZ99333	Aaz99333	DNA encod
38	107.4	37.6	434	3	AAZ99332	Aaz99332	DNA encod
39	107.4	37.6	446	3	AAZ99329	Aaz99329	DNA encod
40	107.4	37.6	485	3	AAZ99335	Aaz99335	DNA encod
41	107.4	37.6	488	3	AAZ99338	Aaz99338	DNA encod
42	107.4	37.6	557	3	AAZ99336	Aaz99336	DNA encod
43	104.8	36.6	1093	3	AAZ99334	Aaz99334	DNA encod
44	76.8	26.9	284	2	AAQ38651	Aaq38651	Truncated
45	76.8	26.9	284	2	AAQ70129	Aaq70129	Antimicro

ALIGNMENTS

RESULT 1
AAT94574
ID AAT94574 standard; cDNA; 286 BP.
XX
AC AAT94574;
XX
DT 12-MAY-1998 (first entry)
XX
DE Alyssum species anti-fungal polypeptide AlyAFP cDNA sequence.
XX
KW Antifungal polypeptide; AlyAFP; inhibition; transgenic plant;
XX phytopathogenic fungus; resistance; ss.
XX Alyssum sp.
XX
FH Key Location/Qualifiers
FT CDS 117..269
FT FT /*tag= a
FT FT /product= "mature AlyAFP protein"
FT FT /note= "no start codon given at 5' end of sequence"
XX
FN WO9737024-A2.
XX
PD 09-OCT-1997.
XX
PF 27-MAR-1997; 97WO-US005709.
XX
PR 29-MAR-1996; 96US-00627706.
XX (MONS) MONGANTO CO.
XX
PI Liang J, Shah D, Wu Y, Rosenberger CA;
XX
DR WPI; 1997-503109/46.
DR P-PSDB; AAW35558.
XX
PT Alyssum antifungal polypeptide and corresponding DNA - used in the
PT production of transgenic plants resistant to phytopathogenic fungi.
XX
PS Claim 12; Page 68; 92pp; English.
XX
CC This sequence encodes the mature protein of an antifungal polypeptide
CC (AlyAFP) isolated from plants of the genus Alyssum. The sequence was PCR
CC amplified using primers AAT94583-T94584, and the resultant 264 bp
CC fragment was cloned as a BamHI fragment into the expression vector
CC pMON23317 to generate plasmid pMON22652. The AlyAFP sequence in this

CC plasmid is placed under control of an E35S promoter and the maize HSP70
 CC intron 1 sequence. The protein can be used to control phytopathogenic
 CC fungi, whilst the DNA can be used to produce transgenic plants that
 CC express the protein making them resistant to the phytopathogenic fungi
 XX
 SQ Sequence 286 BP; 80 A; 62 C; 65 G; 79 T; 0 U; 0 Other;
 Query Match 100.0%; Score 286; DB 2; Length 286;
 Best Local Similarity 100.0%; Pred. No. 4.8e-81;
 Matches 286; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGGAAATCGGATCCCAAGAAAGTAATAGATATGCTTAAGTTTGTCTACCATCACTCTCTTC 60
 Db 1 GGGAAATCGGATCCCAAGAAAGTAATAGATATGCTTAAGTTTGTCTACCATCACTCTCTTC 60
 QY 61 TCTTTGCTGCTCTTCT 120
 Db 61 TCTTTGCTGCTCTTCT 120
 QY 121 TGTGCGAGAGACCAAGTGGGACATGCTCAGGAGTTTGTGGGAACAACAATGCATGCAGGA 180
 Db 121 TGTGCGAGAGACCAAGTGGGACATGCTCAGGAGTTTGTGGGAACAACAATGCATGCAGGA 180
 QY 181 ACCAATGCAGAAACCTTGAAGAGCAGAACACGATCTTGGCAACTATGCTTCCCGAGTTC 240
 Db 181 ACCAATGCAGAAACCTTGAAGAGCAGAACACGATCTTGGCAACTATGCTTCCCGAGTTC 240
 QY 241 ACAATGATTTTGTACTTCCCATGTTAATAAGGATCCGAATTC 286
 Db 241 ACAATGATTTTGTACTTCCCATGTTAATAAGGATCCGAATTC 286

RESULT 2

AAT94582
 ID AAT94582 standard; DNA; 270 BP.

XX
 AC AAT94582;

XX 12-MAY-1998 (first entry)

XX Amplified Alyssum species antifungal polypeptide gene from pMON22652.

XX Antifungal polypeptide; AlyAFP; inhibition; transgenic plant;
 XX phytopathogenic fungus; resistance; ss.

OS Alyssum sp.

XX Key Location/Qualifiers
 FT CDS 22..261

FT sig_peptide /product= "AlyAFP antifungal polypeptide"
 FT 22..108
 FT mat_peptide /tag= b
 FT 109..258
 FT /tag= c

XX WO9737024-A2.

XX 09-OCT-1997.

XX 27-MAR-1997; 97WO-US005709.

XX 29-MAR-1996; 96US-00627706.

XX (MONS) MONSANTO CO.

XX Liang J, Shah D, Wu Y, Rosenberger CA;

XX WPI; 1997-503109/46.

XX P-PSDB; AAW35560.

XX Alyssum antifungal polypeptide and corresponding DNA - used in the
 PT production of transgenic plants resistant to phytopathogenic fungi.

XX Example 4; Page 69; 92pp; English.
 PS
 XX This sequence represents the cDNA sequence cloned into the E. coli
 CC cassette vector pMON2317 to generate vector pMON22652. The cDNA encodes
 CC the antifungal polypeptide AlyAFP, isolated from plants of the genus
 CC Alyssum. The AlyAFP polypeptide can be used to control phytopathogenic
 CC fungi, whilst the coding DNA can be used to produce transgenic plants
 CC that express the polypeptide making them resistant to the phytopathogenic
 CC fungi

XX SQ Sequence 270 BP; 75 A; 58 C; 60 G; 75 T; 0 U; 2 Other;

Query Match 94.1%; Score 269.2; DB 2; Length 270;
 Best Local Similarity 99.3%; Pred. No. 1.1e-75;
 Matches 269; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGATCCAAAGAAAGTAATAGATATGCTTAAGTTTGTACCATCATCTCTCTCTCTCTCTCT 68

Db 1 GGATCCAAASAAAGTAATAGWTATGGCTAAGTTTGTACCATCATCTCTCTCTCTCTCTCT 60

QY 69 GCTCTTGTCT 128

Db 61 GCTCTTGTCT 120

QY 129 AGACCAAGTGGGACATGCTCAGGAGTTTGTGGGAACAACAATGCATGCAGGAACCAATGC 188

Db 121 AGACCAAGTGGGACATGCTCAGGAGTTTGTGGGAACAACAATGCATGCAGGAACCAATGC 180

QY 189 AGAAACCTTGAAGAGCAGAACACGATCTTGGCAACTATGCTTCCCGAGTTCACAAATGT 248

Db 181 AGAAACCTTGAAGAGCAGAACACGATCTTGGCAACTATGCTTCCCGAGTTCACAAATGT 240

QY 249 ATTCTTACTTCCCATGTTAATAAGGATCC 278

Db 241 ATTCTTACTTCCCATGTTAATAAGGATCC 270

RESULT 3

AAT99289
 ID AAT99289 standard; DNA; 481 BP.

XX
 AC AAT99289;

XX 12-MAY-1998 (first entry)

XX Alyssum species AlyAFP cDNA sequence.

XX Antifungal polypeptide; AlyAFP; inhibition; transgenic plant;
 XX phytopathogenic fungus; resistance; ss.

OS Alyssum sp.

XX Key Location/Qualifiers
 FT CDS 53..292

FT sig_peptide /product= "AlyAFP antifungal polypeptide"
 FT 53..139
 FT mat_peptide /tag= b
 FT 140..289
 FT polyA_signal /tag= c
 FT 439..443
 FT /tag= d

XX WO9737024-A2.

XX 09-OCT-1997.

XX 27-MAR-1997; 97WO-US005709.

XX 29-MAR-1996; 96US-00627706.

XX (MONS) MONSANTO CO.

XX	Liang J, Shah D, Wu Y, Rosenberger CA;
PI	WPI; 1997-503109/46.
DR	P-PSDB; AAW35560.
XX	
XX	Alyssum antifungal polypeptide and corresponding DNA - used in the
PT	production of transgenic plants resistant to phytopathogenic fungi.
XX	
XX	Example 4; Fig 1; 92pp; English.
XX	
XX	This sequence represents the cDNA sequence which encodes the antifungal
CC	polypeptide AlyAFP, isolated from plants of the genus Alyssum. The AlyAFP
CC	polypeptide can be used to control phytopathogenic fungi, whilst the
CC	coding DNA can be used to produce transgenic plants that express the
CC	polypeptide making them resistant to the phytopathogenic fungi
XX	
XX	Sequence 481 BP; 147 A; 88 C; 91 G; 154 T; 0 U; 1 Other;
XX	
XX	Query Match 89.8%; Score 256.8; DB 2; Length 481;
XX	Best Local Similarity 99.2%; Pred. No. 1.3e-71;
XX	Matches 256; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX	
QY	11 ATCCAGAAAGTAATAGATATGGCTAAGTTTGCTACCATCATCTCTCTCTTTGCTGC 70
Db	
Db	34 ATCACGAAAGTAATAGATATGGCTAAGTTTGCTACCATCATCTCTCTCTTTGCTGC 93
QY	71 TCTGTCTCTTTGCTGCTCCTTTGAAGCACCACAAATGGTGGATGCAGGTTGTCCGAGAG 130
Db	
QY	94 TCTGTGTTCTCTTTGCTGCTCCTTTGAAGCACCACAAATGGTGGATGCAGGTTGTCCGAGAG 153
QY	131 ACCAAGTGGACATGGTCAGAGTTTCTGGGAAACAACAATGTCATGCAGGAACCAATGCAG 190
Db	
Db	154 ACCAAGTGGACATGGTCAGAGTTTCTGGGAAACAACAATGTCATGCAGGAACCAATGCAG 213
QY	191 AACCTTTGAAGAGCAGAAACACGGATCTTGCAACTATGTTTCCAGCTCAGAAATGAT 250
Db	
Db	214 AACCTTTGAAGAGCAGAAACACGGATCTTGCAACTATGTTTCCAGCTCAGAAATGAT 273
QY	251 TTGTTACTTCCCATGTTAAT 270
Db	
Db	274 TTGTTACTTCCCATGTTAAT 293
XX	
XX	RESULT 4
XX	AAT94581
ID	AAT94581 standard; DNA; 500 BP.
XX	
AC	AAT94581;
XX	
DT	12-MAY-1998 (first entry)
XX	
DE	Composite cDNA sequence for Alyssum species antifungal polypeptide.
XX	
KW	Antifungal polypeptide; AlyAFP; inhibition; transgenic plant;
KW	phytopathogenic fungus; resistance; ss.
XX	
OS	Alyssum sp.
XX	
XX	WO9737024-A2.
PN	
PD	09-OCT-1997.
XX	
XX	27-MAR-1997; 97WO-US005709.
XX	
XX	29-MAR-1996; 96US-00627706.
XX	
PA	(MONS) MONSANTO CO.
XX	
XX	Liang J, Shah D, Wu Y, Rosenberger CA;
PI	WPI; 1997-503109/46.
DR	
XX	

PT	Alyssum antifungal polypeptide and corresponding DNA - used in the production of transgenic plants resistant to phytopathogenic fungi.
XX	
PS	Example 4; Page 67; 92pp; English.
XX	
CC	This sequence represents the cDNA sequence encoding the antifungal polypeptide AlyAPP, from plants of the genus Alyssum. The sequence CC represents a composite of the sequences isolated by 5' and 3' RACE (Rapid Amplification of cDNA Ends) methods (see AAT94577 and AAT94580). The CC AlyAPP polypeptide can be used to control phytopathogenic fungi, whilst CC the coding DNA can be used to produce transgenic plants that express the CC polypeptide making them resistant to the phytopathogenic fungi.
XX	
SQ	Sequence 500 BP; 145 A; 89 C; 111 G; 154 T; 0 U; 1 Other;
	Query Match 75.7%; Score 216.6; DB 2; Length 500;
	Best Local Similarity 91.6%; Pred. No. 9.2e-59;
	Matches 241; Conservative 0; Mismatches 19; Indels 3; Gaps 1
Qy	11 ATCCAAGAAAGTAATAGATATGGCTAAGTTTGTCTACCATCATCTCTCTCTTTGCTGC 70
Dd	50 ATCACGAAGTATATAGATATGGCTAAGTGTCCTCATCATCTCCCTGTCTCTGCTGC 109
Qy	71 TCTTGTCTCTTTTCTGCGCTTTGAAGCACCACAATAATGGTGGATGCA---AGGTTTGGCA 127
Dd	110 TCTTGTCTCTTTCTGCTTTGAAGCACCAGCAATGGTGAGTCACGMAAGTTCTGGCA 169
Qy	128 GAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATGCAGGAACAATG 187
Dd	170 GAGTCCAAAGTGGAAACATGGTCAGCGGTGTGTGGGAATAATAACGCATGCAGGAACCAATG 229
Qy	188 CAGAAACCTTGAAGAAGCAGAACACGGATCTTGCAACTATGTCTTCCCAGCTCACAATG 247
Dd	230 CAGAAACCTTGAAGAGCAGAACACGGATCTTGCACATATGTCTTCCAGCTCACAATG 289
Qy	248 TATTGTGTTACTTCCCATGTTAAT 270
Dd	290 TATTGTGTTACTTCCCATGTTAAT 312
RESULT 5	
AAT94577	ID ID AAT94577 standard; DNA; 308 BP.
XX	
AC	AAT94577;
XX	
DT	12-MAY-1998 (first entry)
XX	
DE	Cloned 5' region of antifungal polypeptide cDNA.
KW	Antifungal polypeptide; AlyAPP; inhibition; transgenic plants;
KW	phytopathogenic fungus; resistance; ss.
XX	
OS	Alyssum sp.
XX	
FN	WO9737024-A2.
XX	
PD	09-OCT-1997.
XX	
PF	27-MAR-1997; 97WO-US005709.
XX	
PR	29-MAR-1996; 96US-00627706.
XX	
PA	(MONS) MONSANTO CO.
XX	
PI	Liang J, Shah D, Wu Y, Rosenberger CA;
XX	
XX	WPI; 1997-503109/46.
XX	
PT	Alyssum antifungal polypeptide and corresponding DNA - used in the production of transgenic plants resistant to phytopathogenic fungi.
XX	
PS	Example 4; Page 65; 92pp; English.

PT	Alyssum antifungal polypeptide and corresponding DNA - used in the
PT	production of transgenic plants resistant to phytopathogenic fungi.
XX	
PS	Example 4; Page 67; 92pp; English.
XX	
CC	This sequence represents the cDNA sequence encoding the antifungal
CC	polypeptide AlyAFP, from plants of the genus Alyssum. The sequence
CC	represents a composite of the sequences isolated by 5' and 3' RACE (Rapid
CC	Amplification of cDNA Ends) methods (see AAT94577 and AAT94580). The
CC	AlyAFP polypeptide can be used to control phytopathogenic fungi, whilst
CC	the coding DNA can be used to produce transgenic plants that express the
CC	polypeptide making them resistant to the phytopathogenic fungi.
XX	
SQ	Sequence 500 BP; 145 A; 89 C; 111 G; 154 T; 0 U; 1 Other;
	Query Match 75.7%; Score 216.6; DB 2; Length 500;
	Best Local Similarity 91.6%; Pred. No. 9.2e-59;
	Matches 241; Conservative 0; Mismatches 19; Indels 3; Gaps 1
Qy	11 ATCCAGAAAGTAATAGATATGGCTAAGTTTGGCTACCATCATCTCTCTCTTTGCTGC 70
Db	50 ATCACGAAAGTATAGATATGGCTAAGTGTGCTTCCATCATCTCCCTGTCTCTGCTGC 109
Qy	71 TCTTGTCTCTTTTCTGCTTGAAGCACCACCAATGGTGGATGCA---AGGTTTGGCA 127
Db	110 TCTTGTCTCTTTTCTGCTTGAAGCACCACCAATGGTGGATGCA---AGGTTTGGCA 169
Qy	128 GAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGACACCAATGCATGCAGGAACCAATG 187
Db	170 GAGTCCCAAGTGGGACATGGTCAGGCGTGTGTGGGAATAATAACGCATGCAGGAACCAATG 229
Qy	188 CAGAAACCTTGAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCAGCTCACAATG 247
Db	230 CAGAAACCTTGAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCAGCTCACAATG 289
Qy	248 TATTGTACTTCCCATGTTAAT 270
Db	290 TATTGTACTTCCCATGTTAAT 312
RESULT 5	
AAT94577	
ID	AAT94577 standard; DNA; 308 BP.
XX	
AC	AAT94577;
XX	
DT	12-MAY-1998 (first entry)
XX	
DE	Cloned 5' region of antifungal polypeptide cDNA.
XX	
KW	Antifungal polypeptide; AlyAFP; inhibition; transgenic plants;
KW	phytopathogenic fungus; resistance; ss.
XX	
OS	Alyssum sp.
XX	
FN	WO9737024-A2.
XX	
PD	09-OCT-1997.
XX	
PF	27-MAR-1997; 97WO-US005709.
XX	
PR	29-MAR-1996; 96US-00627706.
XX	
PA	(MONS) MONSANTO CO.
XX	
FI	Liang J, Shah D, Wu Y, Rosenberger CA;
XX	
XX	WPI; 1997-503109/46.
XX	
PT	Alyssum antifungal polypeptide and corresponding DNA - used in the
PT	production of transgenic plants resistant to phytopathogenic fungi.
XX	
PS	Example 4; Page 65; 92pp; English.
XX	

XX This sequence is the product of the amplification of the 5' region of the
 CC antifungal polypeptide AlyAPP, isolated from plants of the genus *Alyssum*,
 CC by a 5' RACE (Rapid Amplification of cDNA Ends) using primers AAR94575-
 CC T94576). The AlyAPP polypeptide can be used to control phytopathogenic
 CC fungi, whilst the coding DNA can be used to produce transgenic plants
 CC that express the polypeptide making them resistant to the phytopathogenic
 CC fungi
 XX
 SQ Sequence 308 BP; 78 A; 71 C; 78 G; 79 T; 0 U; 2 Other;

Query Match 66.7%; Score 190.8; DB 2; Length 308;
 Best Local Similarity 86.1%; Pred. No. 1.3e-50;
 Matches 223; Conservative 0; Mismatches 33; Indels 3; Gaps 1;
 QY 11 ATCCAGAAAGTAATAGATATGCTTAAGTTTGTACCATCATCTCTCTCTTTGCTGC 70
 DB 50 ATCCAGAAAGTAATAGATATGCTTAAGTTTGTCTTCATCATCTCTCTCTGCTGC 109
 QY 71 TCTTGTCTCTTTGCTGCTTTGAAGCACCACCAATGGTGGATGCA--AGTTTGTGCA 127
 DB 110 TCTTGTCTCTTTGCTGCTTTGAAGCACCACCAATGGTGGATGCA--AGTTTGTGCA 169
 QY 128 GAGACCAAGTGGACATGTCAGGAGTTTGTGGACCAACAAATGATGACGAAACCAATG 187
 DB 170 GAGTCCAAGTGGACATGTCAGGAGTTTGTGGACCAACAAATGATGTCGCAAGATCAGTG 229
 QY 188 CAGAACCTTGAAGACGACACACGATCTTGCACATATGCTTCCAGCTCACAAATG 247
 DB 230 CATTAACCTTGAAGGAGGACGATGCTTGCACATATGCTTCCAGCTCACAAATG 289
 QY 248 TATTTGTTACTTCCCATGT 266
 DB 290 CATATGCTACTTCCCATGT 308

RESULT 6
 AAZ39123
 ID AAZ39123 standard; cDNA to mRNA; 414 BP.
 XX
 AC AAZ39123;
 XX
 DT 15-SEP-2003 (revised)
 DT 01-MAR-2000 (first entry)
 XX
 DE Wasabia japonica antibacterial protein encoding cDNA SEQ ID NO:1.
 XX
 KW Wasabia japonica; antibacterial; food additive; ds.
 XX
 OS Eutrema wasabi.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..243
 FT /*tag= a
 FT /product= "antibacterial protein"
 XX
 JPI133678-A.
 XX
 PD 16-NOV-1999.
 XX
 PF 30-APR-1998; 98JP-00121303.
 XX
 PR 30-APR-1998; 98JP-00121303.
 XX
 PA (IWAT-) IWATE KEN.
 XX
 DR WPI: 2000-057353/05.
 DR P-PSDB; AAY57564.
 XX
 PT An antibacterial protein gene of *Wasabia japonica* - useful as a food- or
 PT feed-additive.
 XX
 PS Claim 3; Page 12-13; 16pp; Japanese.

XX The present sequence encodes an antibacterial protein isolated from
 CC *Wasabia japonica*. The antibacterial protein can be used as a food or feed
 CC additive. (Updated on 15-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 414 BP; 108 A; 79 C; 80 G; 147 T; 0 U; 0 Other;
 XX
 Query Match 62.9%; Score 179.8; DB 3; Length 414;
 Best Local Similarity 84.3%; Pred. No. 4.8e-47;
 Matches 215; Conservative 0; Mismatches 37; Indels 3; Gaps 1;
 QY 30 ATGGCTAAGTTTGTACCATCATCTCTCTCTTTGCTGCTCTTGTCTCTCTCTGCTGC 89
 DB 1 ATGGCTAAGTTTGTCT 60
 QY 90 TTTGAAGCACCACCAATGGTGGATGC--AAGTTTGTGGAGAGACCAAGTGGGACATGG 146
 DB 61 TTTGAAGCACCACCAATGGTGGAGCGCAGAAAGTTGTGGAGAACTCAAGTGGGACATGG 120
 QY 147 TCAGAGTTTGTGGACCAACATCATGTCAGGAAACCAATGACAGAAACCTTGAAGAGCA 206
 DB 121 TCAGAGTCTGTGGAAACCAACATGCGTGCAGAAATCAGTGCATCAACCTTGAGGAGCA 180
 QY 207 GAACACGGATCTTGCAACTATGCTCTTCCAGCTCACAATGATTTGTACTTCCCATGT 266
 DB 181 CGACATGATCTTGCAACTATGCTCTTCCATATCATCATGATGATCTGTTACTTCCCATGT 240
 QY 267 TAATAAGGATCCGAA 281
 DB 241 TAATTAATCTACCAA 255

RESULT 7
 AAQ38650
 ID AAQ38650 standard; DNA; 414 BP.
 XX
 AC AAQ38650;
 XX
 DT 25-MAR-2003 (revised)
 DT 07-JUL-1993 (first entry)
 XX
 DE Rs-APP1 cDNA.
 XX
 KW *Raphanus sativus*; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria;
 KW fungicide; bactericide; antibiotic; antifungal; gram positive;
 KW plant disease resistance; low toxicity.
 XX
 OS *Raphanus sativus*.
 XX
 FH Key Location/Qualifiers
 FT CDS 16..256
 FT /*tag= a
 XX
 PN W09305153-Al.
 XX
 PD 18-MAR-1993.
 XX
 PF 27-AUG-1992; 92WO-GB001570.
 XX
 PR 29-AUG-1991; 91GB-00018523.
 PR 13-FEB-1992; 92GB-00003038.
 PR 25-JUN-1992; 92GB-00013526.
 XX
 PA (ICIL) IMPERIAL CHEM IND PLC.
 XX
 PI Broekaert WF, Cammue BPA, Osborn RW, Rees SB, Terras FRG;
 PI Vanderleyden J;
 XX
 DR WPI: 1993-100978/12.
 XX
 PT Biocidal proteins isolated from seeds of plants - e.g. brassica or
 PT dahlia, useful for increasing plants' resistance to fungal and bacterial
 PT diseases.

XX Example 21; Fig 35; 110pp; English.

XX

XX This cDNA represents the sequence of Rs-AFP1 from *Raphanus sativus*. PCR

CC primer AAQ38640 was used together with AAQ38641 to generate a probe for

CC screening a *Raphanus sativus* seed cDNA library. This primer corresponds

CC to amino acids 2 to 7 of Rs-AFP1 and has a sense orientation. The 143bp

CC product was partially re-amplified using AAQ38542 and AAQ38641 to give a

CC 123bp product, which was further reamplified with the same primers and

CC digoxigenin-11-dUTP instead of dTTP to give a digoxigenin labeled PCR

CC product. This was used to screen a lambda ZAPII cDNA library by in situ

CC plaque hybridisation. Positive plaques were purified and subjected to two

CC additional screening rounds with the same probe. Inserts were excised to

CC rV40 into the pBluescript phagemid form with the aid of helper phage

CC r408. Inserts from 22 positive clones were excised by EcoRI digestion and

CC their size compared by agarose gel electrophoresis. Four clones had

CC insert sizes of approx. 400bp the others between 250-300bp. The inserts

CC of the 4 largest clones were then sequenced and found to differ only in

CC the length of their 5' and 3' UTR's. The longest sequence is given here.

CC (Updated on 25-MAR-2003 to correct PN field.)

XX

XX Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;

XX

[illegible]

RESULT 8	
AAQ70128	
ID	AAQ70128 standard; cDNA; 414 bp.
XX	
AC	AAQ70128;
XX	
DT	25-MAR-2003 (revised)
DT	14-FEB-1995 (first entry)
XX	
DE	Antimicrobial Rs-APPL.
XX	
XX	Antimicrobial; Rs-APPL; symbiosis; disease-resistance; fungus-resistance;
KW	Clavibacter xyli subsp. cynodontis; Cxc; crop improvement; endophyte; ss.
XX	
OS	Raphanus sativus.
XX	
PN	WO9416076-A1.
XX	
PD	21-JUL-1994.
XX	
PF	05-JAN-1994; 94WO-GB0000012.
XX	
PR	08-JAN-1993; 93GB-00000281.
XX	
PA	(ZENE) ZENECA LTD.

Dubock AC, Powell KA, Rees SB;
WPI; 1994-249223/30.
P-PSDB; AARE57325.
Antimicrobial protein producing endo-symbiotic microorganisms - is
produced by combining nucleic acids encoding the protein with an
endophyte, useful for protecting plant hosts from esp. fungal disease.
Disclosure; Page 31; 39pp; English.
Plant-derived antimicrobial proteins are expressed in endosymbiotic
Clavibacter xylis subsp. cynodontis (Cxc). Plants or seeds treated with
recombinant Cxc are protected against fungal disease. A suitable
antimicrobial protein is Rs-Appl from R. sativus. The full-length cDNA
sequence of Rs-Appl is given in AAQ70128. (Updated on 25-MAR-2003 to
correct FN field.)
Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;

Query Match.	62.5%;	Score 178.8;	DB 2;	Length 414;
Best local Similarity	84.3%;	Pred. No. 1e-46;		
Matches 214;	Conservative 0;	Mismatches 37;	Indels 3;	Gaps 1;
Qy	20	AGTAATAGATATGGCTAAGTTTGCTACCATCATCTCTTTCTCTTTTGCTGCTCTTTGTTCT	79	
Db	6	ATTAGTGATCATGGCTAAGTTTGGCTGCATCATCGCACTCTTTTGTGCTGCTCTTTGTTCT	65	
Qy	80	CTTTTGCTGCCCTTTGAGCACCAACAATGGTGGATGCA--AGCTGTGGCGAGACACCAAG	136	
Db	66	TTTTTGCTGCTTTGGAAGCACCAACAATGGTGGAGACACAGAAGTTGTGCGAAGAGCCAAAG	125	
Qy	137	TGGGCATGCTCAGGAGTTTTGTGGGAACAACAATGCATGCAGGAACCAATGCAGAAACCT	196	
Db	126	TGGGCATGCTCAGGAGTCTGTGGAAACAATAACGCAATGCAAGNATCAGTGCATTAACT	185	
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Qy	257	CTTCCCAATGTAAT	270	
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XX	
XX	AC
XX	
DT	25-MAR-2003 (revised)
DT	19-JAN-1998 (first entry)
XX	
XX	
DE	Raphanus sativus antifungal protein I (Rs-AFP1) cDNA.
XX	
XX	
KW	Antifungal protein; candida; fungal resistance; food additive; radish;
KW	crop protection; plant defensin; bacterial protection; preservative; ss.
XX	
OS	Raphanus sativus.
XX	
XX	
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PN	WO9721815-A2.

Defensin; PDF1.1; protection; plant; pathogen; jasmonate; ethylene; fungi; ss.

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Db
142 TGGGACATGGTCAGGGGTTTGGGGAACAGTAATGTCATGCAAGAAATCAGTGCATTAAACCT 201

Db 181 CGACATGATCTTGCACACTATATCTCCCATATACACAGATGATCTGTACTTCTCCCATGT 240

QY 267 TAA 269

Db 241 TAA 243

RESULT 15

ABQ62631
ID ABQ8

AC AB082691:

XX
DT 02-JAN-2003 (first entry)

XX DE Wasabia japonica gamma-thionin encoding cDNA SEQ ID NO:3.

KW Wasabia japonica; gamma-thionin; plant; disease-resistant plant; gene;
XX

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OS	EUCREMA WASABI.
XX	
FH	Key
	Location/Qualifiers

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FT CDS
I. .243
/*tag= a
/product= "gamma-thionin"
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XX
PN
JP2002272292-A.XX
24-SEP-2002XX
PF
22-MAR-2007 : 2007JP-00083526

XX
DP 22 MAY 2001 - 2001 TD 20001500

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XX
XX

DR P-PSDB; ABP53726.

PT A disease-resistant plant in which wasabi gamma-thionin gene is introduced, creation of the disease-resistant plant.

PS Claim 3; Page 8-9; 11pp; Japanese.

The present invention describes a disease-resistant plant in which a wasabi gamma-thionin gene is introduced. Also described is a method for the creation of the above disease-resistant plant by introducing a wasabi gamma-thionin gene to a plant. The present sequence encodes a Eutrema wasabi (Wasabia japonica) gamma-thionin protein from the present invention

Sequence 243 BP: 59 A: 55 C: 55 G: 74 T: 0 U: 0 Other: 0

Query Match 61.5%; Score 175.8; DB 6; Length 243;

Best Local Similarity 85.6%; Pred. No. 7.2e-46;
Matches 208; Conservative 0; Mismatches 32; Indels 3; Gaps 1;

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D**b** 61 TTTGAAGCACCATCAATGGTGAAGCGCAGAAGTTGTGCGAGAAGTCAAGTGGGACATGG 120

QY 147 TCAGGAGTTGTGGGAACAACAATGCATGCAGGAACCAATGCAGAAACCTTGAAAGAGCA 206

Db 121 TCAGGAGTCTGTGGAAACAACAATGCGTGCAGGCATCAGTGCATCAACCTTGAGGGAGCA 180

QY 207 GAACACGGATCTTGCAACTATGTCTTCCAGCTCACAATGTATTTGTTACTTCCCATGT 266

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 18, 2004, 17:08:11 ; Search time 58.5 Seconds
(without alignments)
2713.093 Million cell updates/sec

Title: US-10-681-972-12
Perfect score: 286
Sequence: 1 ggaattcgatccaagaaa.....taataaggatccgaattccc 286

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgm2_6/ptodata/2/ina/5A COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	286	100.0	286	1	US-08-627-706-12
2	286	100.0	286	3	US-09-103-489-12
3	286	100.0	286	4	US-09-829-381D-12
4	269.2	94.1	270	1	US-08-627-706-14
5	269.2	94.1	270	3	US-09-103-489-14
6	269.2	94.1	270	4	US-09-829-381D-14
7	216.6	75.7	500	1	US-08-627-706-9
8	216.6	75.7	500	3	US-09-103-489-9
9	216.6	75.7	500	4	US-09-829-381D-9
10	190.8	66.7	308	1	US-08-627-706-5
11	190.8	66.7	308	3	US-09-103-489-5
12	190.8	66.7	308	4	US-09-829-381D-5
13	178.8	62.5	414	1	US-08-377-687-48
14	178.8	62.5	414	3	US-08-777-192-48
15	178.8	62.5	414	4	US-08-971-982-48
16	178.8	62.5	414	4	US-09-077-951-19
17	178.8	62.5	414	4	US-09-077-948A-45
18	175	61.2	288	1	US-08-377-687-58
19	175	61.2	288	3	US-08-777-192-58
20	175	61.2	288	4	US-08-971-982-58
21	172.2	60.2	285	1	US-08-627-706-16
22	172.2	60.2	285	3	US-09-103-489-16
23	172.2	60.2	285	4	US-09-829-381D-16
24	165.8	58.0	285	1	US-08-627-706-17
25	165.8	58.0	285	3	US-09-103-489-17
26	165.8	58.0	285	4	US-09-829-381D-17
27	112.4	39.3	243	4	US-09-732-210-11

28	111.6	39.0	306	1	US-08-627-706-8	Sequence 8, Appl
29	111.6	39.0	306	3	US-09-103-489-8	Sequence 8, Appl
30	111.6	39.0	306	4	US-09-829-381D-8	Sequence 8, Appl
31	76.8	26.9	284	1	US-08-377-687-50	Sequence 50, Appl
32	76.8	26.9	284	1	US-08-777-192-50	Sequence 50, Appl
33	76.8	26.9	284	3	US-08-971-982-50	Sequence 50, Appl
34	51	17.8	565	4	US-09-589-733C-6	Sequence 6, Appl
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36	40	14.0	40	3	US-09-103-489-11	Sequence 11, Appl
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38	39.8	13.9	150	1	US-08-377-687-31	Sequence 31, Appl
39	39.8	13.9	150	1	US-08-377-687-33	Sequence 31, Appl
40	39.8	13.9	150	1	US-08-377-687-34	Sequence 31, Appl
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42	39.8	13.9	150	1	US-08-777-192-33	Sequence 31, Appl
43	39.8	13.9	150	1	US-08-777-192-34	Sequence 31, Appl
44	39.8	13.9	150	3	US-08-971-982-31	Sequence 31, Appl
45	39.8	13.9	150	3	US-08-971-982-33	Sequence 31, Appl

ALIGNMENTS

RESULT 1
US-08-627-706-12
; Sequence 12, Application US/08627706
; Patent No. 5773696
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yennie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles B. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. 5773696th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/627,706
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21(10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6224
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-627-706-12

Query Match 100.0%; Score 286; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 9.2e-84;
Matches 286; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAATTCGATCCAAAGAAAGTAATAGATATGCTAAGTTTGCTACCATCTCTCTTC 60
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Db 1 GGGAATTCGGATCCAGAAAGTAATAGATATGGCTAAGTTTGTACCATCATCTCTCTTC 60
QY 61 TCTTTGCTGCTCTTGTCTCTTTGCTGCTTGAAGCACCAACAATGGTGGATGCAAGGT 120
Db 61 TCTTTGCTGCTCTTGTCTCTTTGCTGCTTGAAGCACCAACAATGGTGGATGCAAGGT 120
QY 121 TGTGCGAGAGACCAAGTGGGACATGGTCAGAGTTTGTGGGAACAACAATGCATGCAGGA 180
Db 121 TGTGCGAGAGACCAAGTGGGACATGGTCAGAGTTTGTGGGAACAACAATGCATGCAGGA 180
QY 181 ACCAATGCAGAAACCTTGAAGAGACAGAACACCGATCTTGCACATATGTCTTCCAGCTC 240
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QY 241 ACAAAATGATTTGTACTTCCCATGTTAATAAGGATCCGAATTCCTC 286
Db 241 ACAAAATGATTTGTACTTCCCATGTTAATAAGGATCCGAATTCCTC 286

RESULT 2
US-09-103-489-12
; Sequence 12, Application US/09103489
; Patent No. 6215048
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yennie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. 6215048th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/103,489
; FILING DATE: 24-JUN-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21 (10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 537-6224
; TELEFAX: (314) 537-6047
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

US-09-103-489-12
Query Match 100.0%; Score 286; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 9.2e-84;
Matches 286; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGAATTCGGATCCAGAAAGTAATAGATATGGCTAAGTTTGTACCATCATCTCTCTTC 60
Db 1 GGGAATTCGGATCCAGAAAGTAATAGATATGGCTAAGTTTGTACCATCATCTCTCTTC 60
QY 61 TCTTTGCTGCTCTTGTCTCTTTGCTGCTTGAAGCACCAACAATGGTGGATGCAAGGT 120

Db 61 TCTTTGCTGCTCTTGTCTCTTTGCTGCTTGAAGCACCAACAATGGTGGATGCAAGGT 120
QY 121 TGTGCGAGAGACCAAGTGGGACATGGTCAGAGTTTGTGGGAACAACAATGCATGCAGGA 180
Db 121 TGTGCGAGAGACCAAGTGGGACATGGTCAGAGTTTGTGGGAACAACAATGCATGCAGGA 180
QY 181 ACCAATGCAGAAACCTTGAAGAGACAGAACACCGATCTTGCACATATGTCTTCCAGCTC 240
Db 181 ACCAATGCAGAAACCTTGAAGAGACAGAACACCGATCTTGCACATATGTCTTCCAGCTC 240
QY 241 ACAAAATGATTTGTACTTCCCATGTTAATAAGGATCCGAATTCCTC 286
Db 241 ACAAAATGATTTGTACTTCCCATGTTAATAAGGATCCGAATTCCTC 286

RESULT 3
US-09-829-381D-12
; Sequence 12, Application US/09829381D
; Patent No. 6653280
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yennie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alyssum and Methods for Control
; TITLE OF INVENTION: Plant Pathogenic Fungi
; FILE REFERENCE: 38-21 (10700) C
; CURRENT APPLICATION NUMBER: US/09/829,381D
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/103,489
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 286
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic PCR reaction product
US-09-829-381D-12

Query Match 100.0%; Score 286; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 9.2e-84;
Matches 286; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGAATTCGGATCCAGAAAGTAATAGATATGGCTAAGTTTGTACCATCATCTCTCTTC 60
Db 1 GGGAATTCGGATCCAGAAAGTAATAGATATGGCTAAGTTTGTACCATCATCTCTCTTC 60
QY 61 TCTTTGCTGCTCTTGTCTCTTTGCTGCTTGAAGCACCAACAATGGTGGATGCAAGGT 120
Db 61 TCTTTGCTGCTCTTGTCTCTTTGCTGCTTGAAGCACCAACAATGGTGGATGCAAGGT 120
QY 121 TGTGCGAGAGACCAAGTGGGACATGGTCAGAGTTTGTGGGAACAACAATGCATGCAGGA 180
Db 121 TGTGCGAGAGACCAAGTGGGACATGGTCAGAGTTTGTGGGAACAACAATGCATGCAGGA 180
QY 181 ACCAATGCAGAAACCTTGAAGAGACAGAACACCGATCTTGCACATATGTCTTCCAGCTC 240
Db 181 ACCAATGCAGAAACCTTGAAGAGACAGAACACCGATCTTGCACATATGTCTTCCAGCTC 240
QY 241 ACAAAATGATTTGTACTTCCCATGTTAATAAGGATCCGAATTCCTC 286
Db 241 ACAAAATGATTTGTACTTCCCATGTTAATAAGGATCCGAATTCCTC 286

RESULT 4
US-08-627-706-14
; Sequence 14, Application US/08627706
; Patent No. 5773696
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.

APPLICANT: Wu, Yennie S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 5773696th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,706
FILING DATE: 08/06/2004
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21(10700)A
TELEPHONE: (314)537-6224
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 270 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-627-706-14

Query Match 94.1%; Score 269.2; DB 1; Length 270;
Best Local Similarity 99.3%; Pred. No. 2.7e-78;
Matches 268; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY	9	GGATCCAAAGAAAGTAATAGATATGGCTAAGTTGCTACCATCATCTCTCTCTTTGCT	68
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QY	69	GCTCTTGTCTCTTTGCTGCTTTGAAGCACCACCAATGGTGGATGCAAGTTGTGGAG	128
Db	61	GCTCTTGTCTCTTTGCTGCTTTGAAGCACCACCAATGGTGGATGCAAGTTGTGGAG	120
QY	129	AGACCAAGTGGACATGGTCAGGAGTTTGTGGGAAACAATGATGATGCAAGCAATGC	188
Db	121	AGACCAAGTGGACATGGTCAGGAGTTTGTGGGAAACAATGATGATGCAAGCAATGC	180
QY	189	AGAAACCTTCAAGAGCAGACACGAGTCTTGAACACTATCTCTCCAGCTCAAAATGT	248
Db	181	AGAAACCTTGAAGAGCAGACACGAGTCTTGAACACTATCTCTCCAGCTCAAAATGT	240
QY	249	ATTGTGTACTTCCCATGTTAATAGGATCC	278
Db	241	ATTGTGTACTTCCCATGTTAATAGGATCC	270

RESULT 5
US-09-103-489-14
Sequence 14, Application US/09103489
Patent No. 6215048
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yennie S.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi

NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 6215048th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,489
FILING DATE: 24-JUN-1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21(10700)A
TELEPHONE: (314) 537-6224
TELEFAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 270 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-103-489-14

Query Match 94.1%; Score 269.2; DB 3; Length 270;
Best Local Similarity 99.3%; Pred. No. 2.7e-78;
Matches 268; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY	9	GGATCCAAAGAAAGTAATAGATATGGCTAAGTTGCTACCATCATCTCTCTCTTTGCT	68
Db	1	GGATCCAAAGAAAGTAATAGATATGGCTAAGTTGCTACCATCATCTCTCTCTTTGCT	60
QY	69	GCTCTTGTCTCTTTGCTGCTTTGAAGCACCACCAATGGTGGATGCAAGTTGTGGAG	128
Db	61	GCTCTTGTCTCTTTGCTGCTTTGAAGCACCACCAATGGTGGATGCAAGTTGTGGAG	120
QY	129	AGACCAAGTGGACATGGTCAGGAGTTTGTGGGAAACAATGATGATGCAAGCAATGC	188
Db	121	AGACCAAGTGGACATGGTCAGGAGTTTGTGGGAAACAATGATGATGCAAGCAATGC	180
QY	189	AGAAACCTTCAAGAGCAGACACGAGTCTTGAACACTATCTCTCCAGCTCAAAATGT	248
Db	181	AGAAACCTTGAAGAGCAGACACGAGTCTTGAACACTATCTCTCCAGCTCAAAATGT	240
QY	249	ATTGTGTACTTCCCATGTTAATAGGATCC	278
Db	241	ATTGTGTACTTCCCATGTTAATAGGATCC	270

RESULT 6
US-09-829-381D-14
Sequence 14, Application US/09829381D
Patent No. 6653280
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yennie S.
TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Control
TITLE OF INVENTION: Plant Pathogenic Fungi
FILE REFERENCE: 38-21(10700) C
CURRENT APPLICATION NUMBER: US/09/829,381D
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/103,489

;; PRIOR FILING DATE: 1998-06-24
;; NUMBER OF SEQ ID NOS: 20
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 14
;; LENGTH: 270
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Plasmid
US-09-829-381D-14

Query Match 94.1%; Score 269.2; DB 4; Length 270;
Best Local Similarity 99.3%; Pred. No. 2.7e-78;
Matches 268; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 9 GGATCCAAGAAAGTAATAGATATGGCTTAAGTTTGCTACCATCATCTCTCTCTCTTGCT 68
Db 1 GGATCCAAGAAAGTAATAGTATGGCTTAAGTTTGCTACCATCATCTCTCTCTTGCT 60
QY 69 GCTCTTGTTCT 128
Db 61 GCTCTTGTTCT 120
QY 129 AGACCAAGTGGGACATGGTCCAGAGTTTGTGGGACCAACAATGCTGATGCAAGTTTGCGAG 188
Db 121 AGACCAAGTGGGACATGGTCCAGAGTTTGTGGGACCAACAATGCTGATGCAAGTTTGCGAG 180
QY 189 AGAAACCTTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCAGCTCACAATGT 248
Db 181 AGAAACCTTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCAGCTCACAATGT 240
QY 249 ATTGTGTACTTCCCATGTTAATGAAGATCC 278
Db 241 ATTGTGTACTTCCCATGTTAATGAAGATCC 270

RESULT 7
US-08-627-706-9
; Sequence 9, Application US/08627706
; Patent No. 5773696
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. 5773696th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/627,706
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21(10700)A
; TELEPHONE: (314)537-6224
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 500 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

;; LENGTH: 500 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
US-08-627-706-9

Query Match 75.7%; Score 216.6; DB 1; Length 500;
Best Local Similarity 91.6%; Pred. No. 5e-61;
Matches 241; Conservative 0; Mismatches 19; Indels 3; Gaps 1;
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Db 50 ATCAAGAAGTAATAGATATGGCTTAAGTTTGCTACCATCATCTCTCTCTCTTGCTGC 109
QY 71 TCTGTCT 127
Db 110 TCTGTCT 169
QY 128 GAGACCAAGTGGGACATGGTCCAGAGTTTGTGGGACCAACAATGCTGATGCAAGTTTGCGA 187
Db 170 GAGTCCCAAGTGGGACATGGTCCAGAGTTTGTGGGACCAACAATGCTGATGCAAGTTTGCGA 229
QY 188 CAGAAACCTTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCAGCTCACAATG 247
Db 230 CAGAAACCTTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCAGCTCACAATG 289
QY 248 TATTTGTACTTCCCATGTTAAT 270
Db 290 TATTTGTACTTCCCATGTTAAT 312

RESULT 8
US-09-103-489-9
; Sequence 9, Application US/09103489
; Patent No. 6215048
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. 6215048th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/103,489
; FILING DATE: 24-JUN-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21 (10700)A
; TELEPHONE: (314) 537-6224
; TELEFAX: (314) 537-6047
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 500 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/971,982
FILING DATE: 17-No. 6187904-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 414 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 16..255
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-08-971-982-48

Query Match 62.5%; Score 178.8; DB 3; Length 414;
Best Local Similarity 84.3%; Pred. No. 9.7e-49;
Matches 214; Conservative 0; Mismatches 37; Indels 3; Gaps 1;
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QY 80 CTTTGGCTGCTTTGAGCACCACCAATGGTGGATGCA---AGTTTGGGAGAGACCAAG 136
Db 66 TTTTGTGCTTTTGGAGCACCACCAATGGTGGAGCAGCAAGTTTGGCAAGGCCAAG 125
QY 137 TGGGACATGGTCAGGAGTTTGTGGGAACCAACATGATGAGGAGCAACCAATGCAAGAACCT 196
Db 126 TGGGACATGGTCAGGAGTTTGTGGGAACCAACATGATGAGGAGCAACCAATGCAAGAACCT 185
QY 197 TGAAGAGCAGAACACGGATCTTGGCAACTATGTCTTCCAGCTCACAATATGTTTGTGA 256
Db 186 TGAGAAAGCAGCAGATGGATCTTGGCAACTATGTCTTCCAGCTCACAATATGTTTGTGA 245
QY 257 CTTCCCATGTTAAT 270
Db 246 CTTTCCTGTTAAT 259

Search completed: May 18, 2004, 19:02:18
Job time : 59.5 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 18, 2004, 17:59:12 ; Search time 263.25 Seconds
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4930.226 Million cell updates/sec

Title: US-10-681-972-12

Perfect score: 286

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Gapop 10.0 , Gapext 1.0

Searched: 2947334 seqs, 2269024515 residues

Total number of hits satisfying chosen parameters: 5894648

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:**

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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:
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19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	286	100.0	286	13	US-10-681-972-12
3	269.2	94.1	270	9	US-09-829-381A-14
4	269.2	94.1	270	13	US-10-681-972-14
5	216.6	75.7	500	9	US-09-829-381A-9
6	216.6	75.7	500	13	US-10-681-972-9
7	190.8	66.7	308	9	US-09-829-381A-5
8	190.8	66.7	308	13	US-10-681-972-5
9	178.8	62.5	414	9	US-09-759-584-48
10	178.8	62.5	414	13	US-10-388-361A-45
11	178.8	62.5	414	14	US-10-006-252A-19
12	176.6	61.7	403	9	US-09-732-561-13
13	176.2	61.6	400	9	US-09-732-561-15
14	176.2	61.6	400	9	US-09-887-576-607

15	175	61.2	288	9	US-09-759-584-58	Sequence 58, Appl
16	174.2	60.9	243	9	US-09-938-842A-2046	Sequence 2046, Ap
17	174.2	60.9	243	11	US-09-938-842A-2046	Sequence 2046, Ap
18	172.2	60.2	285	9	US-09-829-381A-16	Sequence 16, Appl
19	172.2	60.2	285	13	US-10-681-972-16	Sequence 16, Appl
20	165.8	58.0	285	9	US-09-829-381A-17	Sequence 17, Appl
21	165.8	58.0	285	13	US-10-681-972-17	Sequence 17, Appl
22	120.8	42.2	1616	9	US-09-732-561-21	Sequence 21, Appl
23	111.6	39.0	306	9	US-09-829-381A-8	Sequence 8, Appl
24	111.6	39.0	306	13	US-10-681-972-8	Sequence 8, Appl
25	76.8	26.9	284	9	US-09-759-596-283	Sequence 50, Appl
26	60.6	21.2	373	9	US-09-770-696-283	Sequence 283, Appl
27	51	17.8	439	15	US-10-178-449A-15	Sequence 15, Appl
28	51	17.8	457	15	US-10-178-449A-15	Sequence 15, Appl
29	51	17.8	458	15	US-10-178-449A-21	Sequence 21, Appl
30	51	17.8	460	15	US-10-178-449A-17	Sequence 17, Appl
31	51	17.8	461	15	US-10-178-449A-46	Sequence 46, Appl
32	51	17.8	463	15	US-10-178-449A-9	Sequence 9, Appl
33	51	17.8	464	15	US-10-178-449A-19	Sequence 19, Appl
34	51	17.8	472	15	US-10-178-449A-23	Sequence 23, Appl
35	51	17.8	565	12	US-10-636-396-6	Sequence 6, Appl
36	51	17.8	603	15	US-10-178-449A-11	Sequence 11, Appl
37	49.6	17.3	470	15	US-10-178-213-88	Sequence 88, Appl
38	48	16.8	610	15	US-10-178-449A-29	Sequence 29, Appl
39	48	16.8	658	15	US-10-178-449A-7	Sequence 7, Appl
40	47.4	16.6	529	15	US-10-178-449A-48	Sequence 48, Appl
41	44.8	15.7	579	15	US-10-178-449A-31	Sequence 31, Appl
42	44.6	15.6	501	15	US-10-178-449A-5	Sequence 5, Appl
43	43.6	15.2	156	15	US-10-178-449A-34	Sequence 34, Appl
C 44	40	14.0	40	9	US-09-829-381A-11	Sequence 11, Appl
C 45	40	14.0	40	13	US-10-681-972-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1

US-09-829-381A-12
; Sequence 12, Application US/09829381A
; Patent No. US20020144306A1

GENERAL INFORMATION:
APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yannie S.

TITLE OF INVENTION: Antifungal Polypeptide and Methods for
Controlling Plant Pathogenic Fungi

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. US20020144306A1th
CITY: St. Louis
STATE: Missouri

COUNTRY: USA

ZIP: 63198

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/829,381A

FILING DATE: 09-Apr-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/103,489

FILING DATE: 1998-06-24

ATTORNEY/AGENT INFORMATION:

NAME: Cohen, Charles E.

REGISTRATION NUMBER: 34,565

REFERENCE/DOCKET NUMBER: 38-21 (10700)A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (314) 537-6224

TELEFAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-829-381A-12

Query Match 100.0%; Score 286; DB 9; Length 286;
Best Local Similarity 100.0%; Pred. No. 8.7e-83;
Matches 286; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGAATTCGGATCCAGAAAGTAATAGATATGGCTAAGTTTGTACCATCATCTCTCTTC 60
DB 1 GCGAATTCGGATCCAGAAAGTAATAGATATGGCTAAGTTTGTACCATCATCTCTCTTC 60
QY 61 TCTTTGCTGCTCTTGTCTCTCTTTGCTGCTTTGAGCACCACCAAAATGGTGATGCAAGGT 120
DB 61 TCTTTGCTGCTCTTGTCTCTCTTTGCTGCTTTGAGCACCACCAAAATGGTGATGCAAGGT 120
QY 121 TGTGCGAGAGACCAAGTGGGACATGTGTGAGAGTTTGTGGAAACAACAATGCATGCAGGA 180
DB 121 TGTGCGAGAGACCAAGTGGGACATGTGTGAGAGTTTGTGGAAACAACAATGCATGCAGGA 180
QY 181 ACCAATGCAGAAACCTTTGAAGAGCAGAACACCGATCTTGCACATATGTTCCAGCTC 240
DB 181 ACCAATGCAGAAACCTTTGAAGAGCAGAACACCGATCTTGCACATATGTTCCAGCTC 240
QY 241 ACAATGTATTTGTTACTTCCCATGTTTAATAAGATCCGAATTCCTC 286
DB 241 ACAATGTATTTGTTACTTCCCATGTTTAATAAGATCCGAATTCCTC 286

RESULT 2

US-10-681-972-12
Sequence 12, Application US/10681972
Publication No. US20040064850A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonnie S.
TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alysium and Methods for Control
FILE REFERENCE: 38-21 (10700) C
CURRENT APPLICATION NUMBER: US/10/681,972
PRIOR FILING DATE: 2003-10-09
PRIOR APPLICATION NUMBER: US/09/829,381D
PRIOR FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/103,489
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 286
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic PCR reaction product
US-10-681-972-12

Query Match 100.0%; Score 286; DB 13; Length 286;
Best Local Similarity 100.0%; Pred. No. 8.7e-83;
Matches 286; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGAATTCGGATCCAGAAAGTAATAGATATGGCTAAGTTTGTACCATCATCTCTCTTC 60
DB 1 GCGAATTCGGATCCAGAAAGTAATAGATATGGCTAAGTTTGTACCATCATCTCTCTTC 60
QY 61 TCTTTGCTGCTCTTGTCTCTCTTTGCTGCTTTGAGCACCACCAAAATGGTGATGCAAGGT 120

DB 61 TCTTTGCTGCTCTTGTCTCTCTTTGCTGCTTTGAGCACCACCAAAATGGTGATGCAAGGT 120
QY 121 TGTGCGAGAGACCAAGTGGGACATGTGTGAGAGTTTGTGGAAACAACAATGCATGCAGGA 180
DB 121 TGTGCGAGAGACCAAGTGGGACATGTGTGAGAGTTTGTGGAAACAACAATGCATGCAGGA 180
QY 181 ACCAATGCAGAAACCTTTGAAGAGCAGAACACCGATCTTGCACATATGTTCCAGCTC 240
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QY 241 ACAATGTATTTGTTACTTCCCATGTTTAATAAGATCCGAATTCCTC 286
DB 241 ACAATGTATTTGTTACTTCCCATGTTTAATAAGATCCGAATTCCTC 286

RESULT 3

US-09-829-381A-14
Sequence 14, Application US/09829381A
Patent No. US20020144306A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BBAF
STREET: 700 Chesterfield Village Parkway No. US20020144306A1th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/829,381A
FILING DATE: 09-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/103,489
FILING DATE: 1998-06-24
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-6224
TELEFAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 270 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-829-381A-14

Query Match 94.1%; Score 269.2; DB 9; Length 270;
Best Local Similarity 99.3%; Pred. No. 2.6e-77;
Matches 268; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGATCCAGAAAGTAATAGATATGGCTAAGTTTGTACCATCATCTCTCTCTTCTTCT 68
DB 1 GGATCCAGAAAGTAATAGATATGGCTAAGTTTGTACCATCATCTCTCTCTTCTTCT 60
QY 69 GCTCTTGTCTCTTCTTCTTCTTGTGCTTCTTTGAGCACCACCAAAATGGTGATGCAAGGT 128

Db 61 GCTCTGTGCTCTCTTGTGCTGCTTTGAAGCACCACCAATAGTGGATGCAAGTTGTGCGAG 120
QY 129 AGACCAAGTGGACATGTCAGGAGTTTGGGACACCAATGATGATGAGGACCAATGC 188
Db 121 AGACCAAGTGGACATGTCAGGAGTTTGGGACACCAATGATGATGAGGACCAATGC 180
QY 189 AGAAACCTTTGAAAGAGCAGAACACGGATCTTGGCACTATGCTTCCCAAGCTCACAAATGT 248
Db 181 AGAAACCTTTGAAAGAGCAGAACACGGATCTTGGCACTATGCTTCCCAAGCTCACAAATGT 240
QY 249 ATTTGTACTTCCCATGTTAATAGGATCC 278
Db 241 ATTTGTACTTCCCATGTTAATAGGATCC 270

RESULT 4
US-10-681-972-14
; Sequence 14, Application US/10681972
; Publication No. US20040064850A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Controlling Plant Pathogenic Fungi
; FILE REFERENCE: 38-21 (10700) C
; CURRENT APPLICATION NUMBER: US/10/681,972
; PRIOR FILING DATE: 2003-10-09
; PRIOR FILING DATE: 2001-04-09
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 14
; LENGTH: 270
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid
US-10-681-972-14

Query Match 94.1%; Score 269.2; DB 13; Length 270;
Best Local Similarity 99.3%; Pred. No. 2.6e-77;
Matches 268; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 9 GGATCCAAAGAAAGTAATAGATGGCTAAGTTGGCTACCATCATCTCTCTCTTTGCT 68
Db 1 GGATCCAAAGAAAGTAATAGATGGCTAAGTTGGCTACCATCATCTCTCTCTTTGCT 60
QY 69 GCTCTGTGCTCTCTTGTGCTGCTTTGAAGCACCACCAATGATGATGAGGACCAATGC 128
Db 61 GCTCTGTGCTCTCTTGTGCTGCTTTGAAGCACCACCAATGATGATGAGGACCAATGC 120
QY 129 AGACCAAGTGGACATGTCAGGAGTTTGGGACACCAATGATGATGAGGACCAATGC 188
Db 121 AGACCAAGTGGACATGTCAGGAGTTTGGGACACCAATGATGATGAGGACCAATGC 180
QY 189 AGAAACCTTTGAAAGAGCAGAACACGGATCTTGGCACTATGCTTCCCAAGCTCACAAATGT 248
Db 181 AGAAACCTTTGAAAGAGCAGAACACGGATCTTGGCACTATGCTTCCCAAGCTCACAAATGT 240
QY 249 ATTTGTACTTCCCATGTTAATAGGATCC 278
Db 241 ATTTGTACTTCCCATGTTAATAGGATCC 270

RESULT 5
US-09-829-381A-9
; Sequence 9, Application US/09829381A
; Patent No. US20020144306A1

GENERAL INFORMATION:
APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yonnie S.
Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. US20020144306A1th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/829,381A
FILING DATE: 09-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/103,489
FILING DATE: 1998-06-24
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-6224
TELEFAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 500 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-829-381A-9

Query Match 75.7%; Score 216.6; DB 9; Length 500;
Best Local Similarity 91.6%; Pred. No. 5e-60;
Matches 241; Conservative 0; Mismatches 19; Indels 3; Gaps 1;
QY 11 ATCCAAAGAAAGTAATAGATGGCTAAGTTGGCTACCATCATCTCTCTCTTTGCTG 70
Db 50 ATCCAAAGAAAGTAATAGATGGCTAAGTTGGCTACCATCATCTCTCTCTTTGCTG 109
QY 71 TCTTGTCTCTTTGCTGCTTTGAAGCACCACCAATGATGATGAGGACCAATGC 127
Db 110 TCTTGTCTCTTTGCTGCTTTGAAGCACCACCAATGATGATGAGGACCAATGC 169
QY 128 GAGACCAAGTGGACATGTCAGGAGTTTGGGACACCAATGATGATGAGGACCAATGC 187
Db 170 GATCCAAAGTGGACATGTCAGGAGTTTGGGACACCAATGATGATGAGGACCAATGC 229
QY 188 CAGAAACCTTTGAAAGAGCAGAACACGGATCTTGGCACTATGCTTCCCAAGCTCACAAATGC 247
Db 230 CAGAAACCTTTGAAAGAGCAGAACACGGATCTTGGCACTATGCTTCCCAAGCTCACAAATGC 247
QY 248 TATTGTTACTTCCCATGTTAAT 270
Db 290 TATTGTTACTTCCCATGTTAAT 312

RESULT 6
US-10-681-972-9
; Sequence 9, Application US/10681972
; Publication No. US20040064850A1

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RESULT 8
US-10-681-972-5
; Sequence 5, Application US/10681972
; Publication NO. US20040064850A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yennie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alysium and Methods for Control
; TITLE OF INVENTION: Plant Pathogenic Fungi
; FILE REFERENCE: 38-21 (10700) C
; CURRENT APPLICATION NUMBER: US/10/681,972
; CURRENT FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US/09/829,381D
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/103,489
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 308

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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic PCR reaction product
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (22) ..(248)
; OTHER INFORMATION: N = any nucleotide
US-10-681-972-5

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Query Match	56.7%;	Score 190.8;	DB 13;	Length 308;
Best Local Similarity	86.1%;	Pred. No. 1e-51;		
Matches 223;	Conservative 0;	Mismatches 33;	Indels 3;	Gaps 1;
QY	11	ATCCAGAAAGTAATAGATATGGCTAAGTTTGCTACCATCATCTCTCTCTCTTTGCTGC	70	
Db	50	ATCACAGAAAGTAATAGATATGGCTAAGTTGCTTCATCATCTCCCTGTCTCTGCTGC	109	
QY	71	TCCTGTTCCTTTGCTGCTCCCTTTGAAGACACAAATGGTGGATGCA---AGTTGTGCGA	127	
Db	110	TCCTGTTCCTTTGCTGCTTTTGAAGACACAGCAATGGTGGAGTTCACGGAAATTGCGCA	169	
QY	128	GAGACCAAGTGGACATGGTCAGGAGTTTGTGGGAAACAAATGTCATGTCAGGAACCAATG	187	
Db	170	GAGTCCAAGTGGAAACATGGTCAGGCGTGTGTGGAAACAAATGCTTGCAGAAATCAGTG	229	
QY	188	CAGAAACCTTGAAGAGCAGAAACAGGACTTTGCAACTATGTCTTCCAGCTACAAATG	247	
Db	230	CATTAACCTTGAAGGAGCNCGATGGATCTTGCACATATGTCTTCCAGCTCACAAATG	289	
QY	248	TATTTGTTACTTCCCATGT	266	
Db	290	CATATGCTACTTCCCTGT	308	

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1  RESULT 9
2  US/09-759-584-48
3  / Sequence 48, Application US/09759584
4  / Patent No. US2001014732A1
5  / GENERAL INFORMATION:
6  / APPLICANT: BROKHAERT, WILLEM F.
7  / APPLICANT: CAMMUE, BRUNO P.A.
8  / APPLICANT: OSBORN, ROBERT W.
9  / APPLICANT: REES, SARAH B.
10 / APPLICANT: TERRAS, FRANKY R.G.
11 / APPLICANT: VANDERLEYDEN, JOZEF
12 / TITLE OF INVENTION: BIOCIDAL PRO
13 / NUMBER OF SEQUENCES: 59
14 / CORRESPONDENCE ADDRESS:
15 / ADDRESSEE: CUSHMAN DABRY & CUS
16 / STREET: 1100 NEW YORK AVENUE, I
17 / CITY: WASHINGTON
18 / STATE: D.C.
19 / COUNTRY: USA
20 / ZIP: 20005
21 / COMPUTER READABLE FORM:
22 / MEDIUM TYPE: Floppy disk
23 / COMPUTER: IBM PC compatible
24 / OPERATING SYSTEM: PC-DOS/MS-DOS
25 / SOFTWARE: PatentIn Release #1.0
26 / CURRENT APPLICATION DATA:
27 / APPLICATION NUMBER: US/09/759,5
28 / FILING DATE:
29 / CLASSIFICATION:
30 / PRIOR APPLICATION DATA:
31 / APPLICATION NUMBER: 08/377,687
32 / FILING DATE:
33 / ATTORNEY/AGENT INFORMATION:
34 / NAME: KOKULAS, PAUL N.
35 / REGISTRATION NUMBER: 16,773
36 / REFERENCE/DOCKET NUMBER: 99042
37 / TELECOMMUNICATION INFORMATION:
38 / TELEPHONE: 202-861-3000

```

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; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..255
; US-09-759-584-48

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Query Match	62.5%;	Score 178.8;	DB 9;	Length 414;
Best Local Similarity	84.3%;	Pred. No. 9,7e-48;		
Matches 214;	Conservative 0;	Mismatches 37;	Indels 3;	Gaps 1;
QY	20	AGTAAAGATATGGCTAAAGTTTGGTACCATCACTCTCTTCTCTTTTGGTCTGCTCTGTGTTCT	79	
Db	6	ATTAGTGATCATGGCTAAGTTTGGGTCCATCATCGCACTTCTTTTGTGCTCTGTGTTCT	65	
QY	80	CTTTTGGTGCCTTTGAGCACCACCAATGGTGGATGCA---AGTTGTGCGAGAGACCAAG	136	
Db	66	TTTTTGTCTCTTCGAGAGCACCACCAATGGTGGAGCACAGAAAGTTGTGCGAAAGGCCAAG	125	
QY	137	TGGGCATGCGTCAGGAGTTTGTGGGACCAACAATGCATGCAGCAACCAATGCAGAAACCT	196	
Db	126	TGGGCATGCGTCAGGAGTCTGTGGAAACAATAACGCATGCAGAAATCAGTGCATTACCT	185	
QY	197	TGAAAGCAGCAGACACGGATCTTGCAACTATGCTCTCCAGCTCACAATGTATTGTTA	256	
Db	186	TGAAAGCAGCAGCATGGATCTTGCAACTATGCTCTCCAGCTCACAAGTGTATCTGCTA	245	
QY	257	CTTCCCATGTTAAT	270	
Db	246	CTTTCCTTGTAAAT	259	

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RESULT 10
US/10-388-361A-45
// Sequence 45, Application US/10388361A
// Publication No. US20030226169A1
// GENERAL INFORMATION:
// APPLICANT: Van Amerongen, Aart
// APPLICANT: Fant, Franky
// APPLICANT: Borremaas, Frans
// APPLICANT: De Samblanck, Genoveva
// APPLICANT: Sitjensma, Iolke
// APPLICANT: Mueloen, Robbert
// APPLICANT: Fuijck, Wouter
// APPLICANT: Schaaper, Wilhelmus
// APPLICANT: Broekaaert, Willem
// APPLICANT: Van Gelder, Wilhelmus
// APPLICANT: Rees, Sarah
// TITLE OF INVENTION: Antifungal Proteins
// FILE REFERENCE: 50094PPDDIV
// CURRENT APPLICATION NUMBER: US/10/388,361A
// CURRENT FILING DATE: 2003-03-13
// PRIOR APPLICATION NUMBER: US 09/077,948
// PRIOR FILING DATE: 1998-08-07
// PRIOR APPLICATION NUMBER: PCT/GB96/03068
// PRIOR FILING DATE: 1996-12-12
// PRIOR APPLICATION NUMBER: GB 960552.9
// PRIOR FILING DATE: 1996-03-28
// PRIOR APPLICATION NUMBER: GB 9525455.3
// PRIOR FILING DATE: 1995-12-13
// NUMBER OF SEQ ID NOS: 141
// SOFTWARE: FastSeq for Windows Version 4.0
// SEQ ID NO 45
// LENGTH: 414
// TYPE: DNA
// ORGANISM: Raphanus sativus
US/10-388-361A-45

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Query Match 62.5%; Score 178.8; DB 13; Length 414;
 Best Local Similarity 84.3%; Pred. No. 9.7e-48;
 Matches 214; Conservative 0; Mismatches 37; Indels 3; Gaps 1;

QY 20 AGTAATAGATATGCTAAGTTGGTACATCATCTCTCTTTGCTGCTCTTTGCT 79
 DB 6 ATTAGTATCATGCTAAGTTGGTCCATCATCGCACTTTCTTTTGGCTGCTTTGCT 65

QY 80 CTTTGTGCTCTTTGAAGCACCACCAATGGTGGATGCA--AGGTTGGCGAGACCAAG 136
 DB 66 TTTTGTGCTCTTTGAAGCACCACCAATGGTGGATGCAAGAGTTGGCGAAGGCCAAG 125

QY 137 TGGACATGCTCAGGAGTTGTTGGGAACAACAATGCAATGCAAGCAACCAATGCAAAACCT 196
 DB 126 TGGACATGCTCAGGAGTTGTTGGGAACAACAATGCAATGCAAGCAACCAATGCAAAACCT 185

QY 197 TGAAGAGCAGACACGGATCTTGCACATATGCTTCCAGCTCACAATGTAATTTGTTA 256
 DB 186 TGAGAAAGCAGACATGGATCTTGCACATATGCTTCCAGCTCACAAGTGTATCTGCTA 245

QY 257 CTTCCCATGTTAAT 270
 DB 246 CTTTCTCTGTTAAT 259

RESULT 11
 US-10-006-252A-19
 ; Sequence 19, Application US/10006252A
 ; Publication No. US20020152498A1
 ; GENERAL INFORMATION:
 ; APPLICANT: De Samblanx, Geneveva
 ; APPLICANT: Broekaert, Willem
 ; APPLICANT: Rees, Sarah
 ; TITLE OF INVENTION: Antifungal Proteins
 ; FILE REFERENCE: SVN-034DV
 ; CURRENT APPLICATION NUMBER: US/10/006,252A
 ; CURRENT FILING DATE: 2001-12-04
 ; PRIOR APPLICATION NUMBER: 09/077,951
 ; PRIOR FILING DATE: 1998-06-10
 ; PRIOR APPLICATION NUMBER: GB 9525474.4
 ; PRIOR FILING DATE: 1995-12-13
 ; PRIOR APPLICATION NUMBER: PCT/GB96/03065
 ; PRIOR FILING DATE: 1996-12-12
 ; NUMBER OF SEQ ID NOS: 77
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 19
 ; LENGTH: 414
 ; TYPE: DNA
 ; ORGANISM: Raphanus sativus
 US-10-006-252A-19

Query Match 62.5%; Score 178.8; DB 14; Length 414;
 Best Local Similarity 84.3%; Pred. No. 9.7e-48;
 Matches 214; Conservative 0; Mismatches 37; Indels 3; Gaps 1;

QY 20 AGTAATAGATATGCTAAGTTGGTACCAATCATCTCTCTTTGCTGCTCTTTGCT 79
 DB 6 ATTAGTATCATGCTAAGTTGGTCCATCATCGCACTTTCTTTTGGCTGCTTTGCT 65

QY 80 CTTTGTGCTCTTTGAAGCACCACCAATGGTGGATGCA--AGGTTGGCGAGACCAAG 136
 DB 66 TTTTGTGCTCTTTGAAGCACCACCAATGGTGGATGCAAGAGTTGGCGAAGGCCAAG 125

QY 137 TGGACATGCTCAGGAGTTGTTGGGAACAACAATGCAATGCAAGCAACCAATGCAAAACCT 196
 DB 126 TGGACATGCTCAGGAGTTGTTGGGAACAACAATGCAATGCAAGCAACCAATGCAAAACCT 185

QY 197 TGAAGAGCAGACACGGATCTTGCACATATGCTTCCAGCTCACAATGTAATTTGTTA 256
 DB 186 TGAGAAAGCAGACATGGATCTTGCACATATGCTTCCAGCTCACAAGTGTATCTGCTA 245

QY 257 CTTCCCATGTTAAT 270

Db 246 CTTTCTCTGTTAAT 259

RESULT 12
 US-09-732-561-13
 ; Sequence 13, Application US/09732561
 ; Patent No. US20020035738A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Thoma, Bart
 ; APPLICANT: Terras, Franky
 ; APPLICANT: Penninckx, Iris
 ; APPLICANT: Manners, John
 ; APPLICANT: Kazan, Kemal
 ; APPLICANT: Broekaert, Willem
 ; TITLE OF INVENTION: Plant Protection Method
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: ZENECA Ag Products
 ; STREET: 1800 Concord Pike
 ; CITY: Wilmington
 ; STATE: DE
 ; COUNTRY: USA
 ; ZIP: 19850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/732,561
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/202,638
 ; FILING DATE:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/GB97/01672
 ; FILING DATE: 20-JUN-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hohenschutz, Liza D.
 ; REGISTRATION NUMBER: 33,712
 ; REFERENCE/DOCKET NUMBER: PPD 50165/UST
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (302) 886-1699
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 403 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; ORIGINAL SOURCE:
 ; STRAIN: PDF 1.1
 US-09-732-561-13

Query Match 61.7%; Score 176.6; DB 9; Length 403;
 Best Local Similarity 83.5%; Pred. No. 5e-47; Mismatches 213; Conservative 0; Indels 3; Gaps 1;

QY 19 AGTAATAGATATGCTAAGTTGGTACCAATCATCTCTCTTTGCTGCTCTTTGCT 78
 DB 15 AAACAATAGTATGCTAAGTCTGTACCATCGTTACTTTCTTCGCTGCTTTGTT 74

QY 79 TCTTTGCTGCCCTTTGAAGCACCACCAATGGTGGATGCA--AGGTTGGCGAGACCAAG 135
 DB 75 TCTTTGCTGCTCTTTGAAGCACCACCAATGGTGGATGCAAGAGTTGGCGAGACCAAG 134

QY 136 GTGGACATGCTCAGGAGTTGTTGGGAACAACAATGCAATGCAAGCAACCAATGCAAAACCT 195
 DB 135 GTGGACATGCTCAGGAGTTGTTGGGAACAACAATGCAATGCAAGCAACCAATGCAAAACCT 194

QY 196 TTGAAGAGCAGACACCGATCTTGCACATATGCTTCCAGCTCACAATGTAATTTGTT 255

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Job time : 264.25 secs

Query Match	61.2%;	Score 175;	DB 9;	Length 288;
Best Local Similarity	83.1%;	Pred. No. 1.4e-46;		
Matches 212;	Conservative 0;	Mismatches 40;	Indels 3;	Gaps 1;

QY	20	AGTAATAGATATCGCTAAGTTTGCTACCATCATCTCTCTCTCTTTGCTGCTGTGTCT	79
Db			
Db	33	ATTAGTGATCATGGCTAAGTTTGGTTCATCATCGCACTCTCTTTTGTCTGCTTGTCT	92
QY	80	CTTTGTCTGCTTTGGAAGCACCAACAATGGTGGATGCA--AGTTGTGCGAGAGACCAAG	136
Db			
Db	93	TTTTTGTCTTTGGAAGCACCAACAATGGTGGAGCACAGAAGTTGTGCCAAGGCCAAG	152
QY	137	TGGGACATGCTCAGGAGTTTGTGGAAACAACAATGCATGCAGGAACCAATGCAGAACCT	196
Db			
Db	153	TGGGACATGCTCAGGAGTCTGTGGAAACAATACGCATGCAAGAACTCAGTGCATTAGACT	212
QY	197	TGAAGAGCAGAACACGGATCTTTCGCACTATGCTTCCAGCTCACAAATGTATTGTGA	256
Db			
Db	213	TGAGAAAGCACGACATGGATCTTGCACATATGCTTCCAGCTCACAAATGTATTGTGA	272
QY	257	CTTCCCATGTTTAATA	271
Db	273	CTTTCCCTTGTTAATA	287

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)
3586.070 Million cell updates/sec

Title: US-10-681-972-12

Perfect score: 286

Sequence: 1 ggggaattggatccaagaaa.....taataaggatccgaattccc 286

Scoring table:

IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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8: em_hcc:*

9: gb_est1:*

10: gb_est2:*

11: gb_hcc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

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22: em_gss_mam:*

23: em_gss_mus:*

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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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5	177.8	62.2	452	14	CD832071
6	177.8	62.2	458	14	CD834994
7	177.8	62.2	470	14	CD831680
8	177.2	62.0	394	12	BG321454
9	176.6	61.7	422	9	AV787956
10	176.2	61.6	400	14	T04323
11	176.2	61.6	408	14	CD833779
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13	176.2	61.6	420	14	CD833944
14	176.2	61.6	421	14	CD826491
15	176.2	61.6	421	14	CD831111
16	176.2	61.6	421	14	CD833977
17	176.2	61.6	422	14	CD833983
18	176.2	61.6	426	14	CD827413
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26	174.6	61.0	418	14	CD832625
27	174.6	61.0	419	14	CD834168
28	174.6	61.0	438	14	CD831294
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31	173	60.5	421	14	CD837517
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38	167.6	58.6	448	14	CD837568
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43	166	58.0	457	14	CD831392
44	165	57.7	422	9	AV789144
45	164.6	57.6	421	9	AV789824

ALIGNMENTS

RESULT 1
BG321515

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BG321515 410 bp mRNA linear EST 27-FEB-2001
Ds01.08a06.R Ds01.AAFC ECORC cold stressed Flixweed seedlings
Descurainia sophia cDNA clone Ds01.08a06, mRNA sequence.

BG321515

BG321515.1 GI:13151193

EST.

Descurainia sophia

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Descurainia.

1 (bases 1 to 410)

Singh, J.A., Piche, C., Couroux, P., De Moors, A., Harris, L.J.,

Hattori, T., Ouellet, L., Robert, L.S., Sprout, D. and Tinker, N.A.

Expressed Sequence Tags from Cold-Stressed Descurainia sophia

Seedlings

Unpublished (2001)

Contact: Singh, J.A.

Eastern Cereal and Oilseed Research Centre

Agriculture and Agri-food Canada

KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A

OC6, Canada

Tel: (613) 759-1662

Fax: (613) 759-1701

Email: singhja@em.agr.ca.

```

FEATURES
  source
    Location/Qualifiers
      1. .410
        /organism="Descurainia sophia"
        /mol_type="mRNA"
        /db_xref="taxon:89411"
        /clone="Ds01_08a06"
        /tissue_type="leaf, stem"
        /dev_stage="1-month seedlings - 1 cm tall - 8 leaf"
        /clone_lib="Ds01_AAFD_EC0RC_cold_stressed_Flixweed_seedlin
        gs"
        /note="Vector: Bluescript SK+/XhoI-EcoRI; Site_1: Eco RI;
        Site_2: Xho I; Plants were grown for 1 month at 20°C/16
        hrs light/day (average 8 leaves, 1 cm tall, weight
        0.02g/plant). Then they were exposed to 20°C, 12 hrs
        light/day, for 1 week. Library prepared by C. Piche using
        Stratagene kit."
      64.0%; Score 183; DB 12; Length 410;
      Best Local Similarity 81.0%; Pred. No. 2.2e-39;
      Matches 205; Conservative 6; Mismatches 42; Indels 0; Gaps 0;

ORIGIN
  Query Match 64.0%; Score 183; DB 12; Length 410;
  Best Local Similarity 81.0%; Pred. No. 2.2e-39;
  Matches 205; Conservative 6; Mismatches 42; Indels 0; Gaps 0;

  QY 18 AAAGTATAGATAGGCTAGTTGCTACCATCATCTCTCTCTTTGCTGCTCTTT 77
  Db 13 ATATATATCATGCTAGTCTAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 72
  QY 78 CTCTTGTCTGCTTTGAAGCACCACCAATGCTGATGCAAGGTTGTCGAGAGACCAAGT 137
  Db 73 CTCTTGTCTGCTTTGAAGCACCACCAATGCTGATGCAAGGTTGTCGAGAGACCAAGT 132
  QY 138 GGCACATGTCAGAGTTTGTGGACACCAATGCTGATGCAAGGTTGTCGAGAGACCAAGT 197
  Db 133 GGCACATGTCAGAGTTTGTGGACACCAATGCTGATGCAAGGTTGTCGAGAGACCAAGT 192
  QY 198 GAAAGAGCAGAACACGATCTTGCACATGCTTCCACGCTCAGCAATGCTATTTGCTAC 257
  Db 193 TAGAGAGCACAATGATCTTGCACATGCTTCCACGCTCAGCAATGCTATTTGCTAC 252
  QY 258 TTCCCATGTTAAT 270
  Db 253 TTCCCATGTTAAT 265

RESULT 2
CB263345
LOCUS
DEFINITION
  25-BB974-008-017-A07-pB12 MP12-ADIS-008 Arabidopsis thaliana cDNA
  clone MP12p76A0717Q 5-PRIME, mRNA sequence.
ACCESSION
  CB263345
VERSION
  CB263345.1 GI:32888118
KEYWORDS
  EST
SOURCE
  Arabidopsis thaliana (thale cress)
  Arabidopsis thaliana
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
  1 (bases 1 to 441)
  Schmidt,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T.,
  Mitchell-Olds,T. and Weisshaar,B.
  Large-scale identification and analysis of genome-wide
  single-nucleotide polymorphisms for mapping in Arabidopsis thaliana
  Genome Res. 13 (6), 1250-1257 (2003)
  22683290
  12799357
  Contact: Weisshaar B
  ADIS DNA core facility at MP12
  Max-Planck-Institute for Plant Breeding Research
  Carl-von-Linne Weg 10, 50829 Koeln, Germany
  Fax: 00492215062851
  Email: weisshaar@piz-koeln.mpg.de
  Insert Length: 441 Std Error: 0.00
  Plate: 17 row: A column: 07
  Seq primer: pB12; GGTGGCGCGCTCTAG.

REFERENCE
  AUTHORS
  TITLE
  JOURNAL
  MEDLINE
  PUBMED
  COMMENT
    Contact: Weisshaar B
    ADIS DNA core facility at MP12
    Max-Planck-Institute for Plant Breeding Research
    Carl-von-Linne Weg 10, 50829 Koeln, Germany
    Fax: 00492215062851
    Email: weisshaar@piz-koeln.mpg.de
    Insert Length: 441 Std Error: 0.00
    Plate: 17 row: A column: 07
    Seq primer: pB12; GGTGGCGCGCTCTAG.

FEATURES
  source
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      1. .441
        /organism="Arabidopsis thaliana"
        /mol_type="mRNA"
        /cultivar="C24"
        /db_xref="GABI:599658"
        /db_xref="taxon:3702"
        /clone="MP12p76A0717Q"
        /tissue_type="seedling"
        /dev_stage="few days old seedlings"
        /lab_host="E. coli XL1-Blue MRF"
        /clone_lib="MP12-ADIS-008"
        /note="Vector: pBluescript SK (-); Site_1: EcoRI; Site_2:
        XhoI; cDNA library from Arabidopsis thaliana, accession
        C24; seedling; Lambda ZAPII phage library was made at the
        Max-Planck-Institute of Molecular Plant Physiology, Golem,
        Germany and mass-excised at the Max-Planck-Institute for
        Plant Breeding Research, Cologne, Germany; cloning sites
        EcoRI-XhoI; Note: Sequencing granted in the context of the
        GABI Arabidopsis Verbund I; Genetic Diversity,
        'Establishment of high-efficiency SNP-based mapping tools
        and development of methods for genome-wide mutation
        detection' PI: Bernd Weisshaar Sequence submission managed
        by RZPD/GABI-Primary database; http://gabi.rzpd.de This
        clone is available from RZPD; contact RZPD (clone@rzpd.de)
        for further information."
      62.2%; Score 177.8; DB 14; Length 441;
      Best Local Similarity 84.2%; Pred. No. 6e-38;
      Matches 213; Conservative 0; Mismatches 37; Indels 3; Gaps 1;

ORIGIN
  Query Match 62.2%; Score 177.8; DB 14; Length 441;
  Best Local Similarity 84.2%; Pred. No. 6e-38;
  Matches 213; Conservative 0; Mismatches 37; Indels 3; Gaps 1;

  QY 20 AGTAATAGATAGGCTAGTTGCTACCATCATCTCTCTCTTTGCTGCTCTTTGTTCT 79
  Db 15 ATATATCATCATGCTAGTCTTCTTCCATCATCACCCTTATCTCGCTGCTCTGTTCT 74
  QY 80 CTCTTGTCTGCTTTGAAGCACCACCAATGTTGGATGCA--AGTTTGTGGAGACCAAG 136
  Db 75 CTCTTGTCTGCTTTGAAGCACCACCAATGTTGGATGCA--AGTTTGTGGAGACCAAG 134
  QY 137 TGGACATGCTCAGGAGTTTGTGGACCAACCAATGATGATGATGATGATGATGATGATGAT 196
  Db 135 TGGACATGCTCAGGAGTTTGTGGACCAACCAATGATGATGATGATGATGATGATGATGAT 194
  QY 197 TGAAGAGCAGAACACGATCTTGCACATGCTTCCACGCTCAGCAATGATGATGATGATGATGAT 256
  Db 195 TGAAGAGCAGAACACGATCTTGCACATGCTTCCACGCTCAGCAATGATGATGATGATGATGAT 254
  QY 257 CTCTCCATGTTAA 269
  Db 255 CGTCCCATGTTAA 267

RESULT 3
CB2634068
LOCUS
DEFINITION
  BN45.040H17F011019 BN45 Brassica napus cDNA clone BN45040H17, mRNA
  sequence.
ACCESSION
  CB2634068
VERSION
  CB2634068.1 GI:32516008
KEYWORDS
  EST.
SOURCE
  Brassica napus (rape)
  Brassica napus
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
  1 (bases 1 to 446)
  Genoplante.
  Genoplante, a major partnership french program in plant genomics
  Unpublished (2003)
  JOURNAL
  COMMENT
    Contact: Genoplante
    Genoplante
    93, rue Henri Rochefort 91025 EVRY CEDEX France

```


80	CTTTGCTGCCTTTTGAAGCA	CAA	CAATGGTGGATGCA	---	AGTTTGCGAGAGACCAAG	136
120	TTTTCGCTGCTTTTCGAAGC	ACC	CAACAAATGGTGGAAAG	CA	CAGAAGTTGTCGAGAGAGCCCAAG	179
137	TGGGACATGTCAGGAGT	TTT	TGGGGAACA	CA	AATGCATGCGAGGACCAATCGAGNAACCT	196
180	TGGACATGGTCAGGAGT	CT	TGTGAAACA	ATA	TACGCATGCAAGCAATCAAGTCATTAACT	239
197	TGAAGAGCAGAA	C	CGGATCTT	TGC	AACATATGTTCCAGCTCACA	256
240	TGAGAAAGC	CG	CATGGA	CTT	TGCAACTATGTTCCAGCTCACA	299
257	CTTCCCA	TGTTAA	269			
300	CTTCCCT	TGTTAA	312			

RESULT 6	CD834994	458 bp	mrna	linear	EST 10-JUL-2003			
LOCUS	BN45.043006F011229	BN45	Brassica napus	cdna clone	BN45043006, mRNA			
DEFINITION	sequence.							
ACCESSION	CD834994							
VERSION	CD834994.1	GI:32516934						
KEYWORDS	EST.							
SOURCE	Brassica napus (rape)							
ORGANISM	Brassica napus							
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;							
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;							
	rosids; eucosids II; Brassicales; Brassicaceae; Brassica.							
	(bases 1 to 458)							

TITLE
JOURNAL
COMMENT

Genoplate, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplate
Genoplate
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplate' (<http://www.genoplate.com>
and <http://genoplate-info.infobiogen.fr>).

```

FEATURES
source
1. .458
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN45043006"
/tissue_type="seed"
/clone_lib="BN45"

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ORIGIN
Query Match          62.2%;   Score 177.8;   DB 14;   Length 458;
Best Local Similarity 84.2%;   Pred. No. 6e-38;
Matches 213; Conservative 0; Mismatches 37; Indels 3; Gaps 1;
/clone_lib="BN45"

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20	AGTAATAGATATGGCTAAAGTTTCTACTACCATCATCTCTTCTCTTTGCTGCTCTTGTCT	79
56	ACTAGTGACATGGCTAAAGTTTCTCTTCCATCAATGGCCCACTTTTCTGCTCTTGTCT	115
80	CTTTGCTGCTTTGAAGCACCAACAATGGTGGATGCA--AGGTTGGCCAGAGACCCAAAG	136
116	TTTCGCTGCTTTCGAAGCACCAACAATGGTGGAGACACAAGTTGTGCAGAGGGCCAAAG	175

137	TGGGACATGGTCAGGAGTTTGTGGGAACAACAAATGATGCAGGAACCAATGCAGAAACCT	196
176	TGGGACATGGTCAGGAGTCTGTGGAAACAATAACGGATGCAGGAATCAGTGCATTAACT	235
197	TGAAGAGCAGAACACGGATCTTGGCAACTATGTCTCCAGCTCACAATAATGTAATTGTTA	256
236	TGAGAAAGCAGCATGGATCTTGGCAACTATGTCTCCAGCTCACAAGTGTATTTGCTA	295

Qy	257	CTTCCCA ⁺ GTAA	269
	296	CTTCCCT ⁺ GTAA	308
Db			

[illegible]

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 470)

REFERENCE

Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91035 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (<http://www.genoplante.com>
and <http://genoplante-info.infobiogen.fr>).

```

source
1 35470
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN4006H13"
/tissue_type="seed"
/clone_lib="BN40"

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Query Match	62.2%	Score 177.8;	DB 14;	Length 470;
Best Local Similarity	84.2%;	Pred. No. 6e-38;		
Matches 213;	Conservative	0;	Mismatches 37;	Indels 3;
				Gaps 1;

QY	20	AGTAATAGATATGGCTAAGTTTGCACCAATCATCTCTTCCTTTCTGCTCTTGTTCT	79
Db	78	ACTAGTAGCATGGCTAAGTTTGTCCATATTGCCCACTTTTTCGCTCGCTTCTTCT	127

80 CTTTCTGCTTTGAAGCACCACCAATGCTGGATGCA---AGTTCTTCGAGAGACCCAAG 136
| | | | |
138 TTTCCTGTGTTTCGAAAGCACCACCAATGTGGAAGCACAGAAGTTGTGCAGAGGCCAAG 197

137 TGGGACATGGTCAGCAGTTTGTGGGAAACAACAATGCATGCAGGAACAATGCAGAAACCT 196 QY
198 TGGGACATGGTCAGCAGTTGTGGGAAACAATACGCATGCAGGAATCAGTGCATTAACT 257 Db

OY
197 TGAAGACGAGAACCGGATCTTGCAACTATCTTCTCCAGGTCAAAATGTATTGTTA 256
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db
258 TGAGAAAGCACGACATGGATCTTGCACATATCTTCTCCAGGTCAAGTGTATTGCTA 317

Qy	257	CTTCCCATGTTAA	269
Db	318	CTTCCCTTGTAA	330

RESULT 8
BG321454 LOCUS
BG321454 DEFINITION
Dso1_08h05_A Dso1_AAFC ECORC cold stressed flkweed seedlings
Descurainia sophia cDNA clone Dso1_08h05, mRNA sequence.
BG321454 ACCESSION
BG321454 VERSION
BG321454.1 GI:13151132
394 bp mRNA linear EST 27-FEB-2001

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 422)
Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y. and Shinozaki, K.
Large scale analysis of Arabidopsis full-length cDNA (2002b)
Unpublished (2002)
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). This clone is in a modified pluscript vector as a SstI/XhoI insert. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for

FEATURES	source	Location/Qualifiers
		1..422
		/organism="Arabidopsis thaliana"
		/mol_type="mRNA"
		/db_xref="taxon:3702"
		/clone="RAFL06-77-K06"
		/dev_stage="plants at various developmental stages from germination to mature seeds"
		/lab_host="DH10B"
		/clone_lib="RAFL6"
		/note="Site 1: SsII; Site 2: XhoI; subjected to dehydration (1, 2, 5, 10, 24 hr) treatments"

ORIGIN	Query Match	61.7%;	Score 176.6;	DB 9;	Length 422;
	Best Local Similarity	83.5%;	Pred. No. 1.3e-37;		
	Matches 213;	Conservative 0;	Mismatches 39;	Indels 3;	Gaps 1;
QY	19	AAGTAATAGATAGCTAAGTTTGCTACCATCATCTCTTCTCTTTGGCTGCTCTTGTTC	78		
Db	392	AAACAATAGTCATGGCTAAGCTGCTACATCGTTACTCTTTCTTCGCTGCTCTTGT	333		
QY	79	TCTTTGCTGCCCTTTGAAGCACCACAAATGGTGGATGCA--AGGTTGTGCGAGAGACCAA	135		
Db	332	TCTTTGCTGCTCTTGAAGCACCAGATGGTGTGGGAAGCACAGAGTTGTGCGAGAGCCAA	273		
QY	136	GTGGACATGCTGCTAGGAGTTTGTGGGAACAACAATGCATGCAGGAACCAATGCAGAAACC	195		
Db	272	GTGGACATGCTCCGAGTTTGTGGGAACAACAATGCATGCAGGAACCAATGCAGTAACC	213		
QY	196	TTGAAAGACGAGAACACGGATCTTGGCAACTATGCTTCCGAGCTCACAAATGATTTGTT	255		
Db	212	TTGAAAGACGAGAACATGGATCTTGGCAACTATGCTTCCGAGCTCACAAATGATCTGCT	153		
QY	256	ACTTCCCATGTTTAAT	270		
Db	152	ACTTCCCATGTTTAAT	138		

RESULT	10
LOCUS	T04323
DEFINITION	T04323 370 Lambda-PRL2 Arabidopsis thaliana cDNA clone 37F10T7, mRNA sequence.
ACCESSION	T04323
VERSION	T04323.1 GI:315483
KEYWORDS	EST.
SOURCE	Arabidopsis thaliana (thale cress)
ORGANISM	Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 400)
 Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomas, M., Retzel, E., and Somerville, C.
 Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones
 Plant Physiol. 106, 1241-1255 (1994)
 95148729
 MEDLINE
 PUBMED
 7846151
 COMMENT
 Contact: Thomas Newman
 MSU-DOE Plant Research Laboratory
 Michigan State University
 MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E. Lansing, MI
 Tel: 517-353-0854
 Fax: 517-353-9168
 Email: 22313tcn@bm.cl.msu.edu
 Seq primer: T7 dye primer.
 Location/Qualifiers
 1. 400
 /organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /strain="var columbia"
 /db_xref="taxon:3702"
 /clone="37F107"
 /clone_lib="Lambda-PRL2"
 /note="Vector: lambda Zip-Lox; Site 1: Sal; Site 2: Not; Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark- rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques). The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dt primed cDNA."
 ORIGIN
 Query Match 61.6%; Score 176.2; DB 14; Length 400;
 Best Local Similarity 83.8%; Pred. No. 1.6e-37;
 Matches 212; Conservative 0; Mismatches 38; Indels 3; Gaps 1;
 QY 20 AGTAATAGATATGGTGAAGTTGGTACCATCATCTCTCTTTCTTGTGCTCTTGTCT 79
 Db 22 AATAATCATCATGGTGAAGTTTGGTCCATCATCACCCCTTATCTTGTGCTCTTGTCT 81
 QY 80 CTTTGTGCTCTTGAAGCACCACCAATGGTGGATGCA---AGGTTGCGAGAGACCAAG 136
 Db 82 CTTTGTGCTCTGACGACCGGCAATGGTGGAGACACAGAAGTTGGGAGAGCCAAAG 141
 QY 137 TGGGACATGGTACAGGAGTTTGGGAAACCAATGCATGCAGGAACCAATGCAGAAACCT 196
 Db 142 TGGGACATGGTACAGGAGTTTGGGAAACCAATGCATGCAGGAATGCATGAATTAACCT 201
 QY 197 TGAAGACAGAACACAGGATCTTGGCAATATGCTTCCAGCTCACAATGTATTGTGTTA 256
 Db 202 TGAAGAGCAACCAATGATGATGCAATATGCTTCCAGCTCACAATGTATTGTGTTA 261
 QY 257 CTTCCCATGTTAA 269
 Db 262 CTTCCCATGTTAA 274
 RESULT 11
 CD833779
 LOCUS
 DEFINITION
 BN45.001115F010914 BN45 Brassica napus cDNA clone BN4500115, mRNA sequence.
 ACCESSION
 CD833779
 VERSION
 CD833779.1 GI:32515719
 KEYWORDS
 EST.
 CD833779
 408 bp mRNA linear EST 10-JUL-2003
 DEFINITION
 BN45.001115F010914 BN45 Brassica napus cDNA clone BN4500115, mRNA sequence.
 ACCESSION
 CD833779
 VERSION
 CD833779.1 GI:32515719
 KEYWORDS
 EST.

Brassica napus (rape)
 Brassica napus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica. 1 (bases 1 to 408)
 Genoplante.
 Genoplante, a major partnership french program in plant genomics
 Unpublished (2003)
 Contact: Genoplante
 Genoplante
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10
 This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (<http://www.genoplante.com>) and <http://genoplante-info.inbio.gen.fr>.
 Location/Qualifiers
 1. 408
 /organism="Brassica napus"
 /mol_type="mRNA"
 /cultivar="Jet neuf"
 /db_xref="taxon:3708"
 /clone="BN4500115"
 /tissue_type="seed"
 /clone_lib="BN45"
 ORIGIN
 Query Match 61.6%; Score 176.2; DB 14; Length 408;
 Best Local Similarity 83.8%; Pred. No. 1.6e-37;
 Matches 212; Conservative 0; Mismatches 38; Indels 3; Gaps 1;
 QY 20 AGTAATAGATATGGTGAAGTTGGTACCATCATCTCTCTTTCTTGTGCTCTTGTCT 79
 Db 18 ACTAGTGACATGGTGAAGTTTGGTCCATCATGCCCCACATTTTGTGCTCTTGTCT 77
 QY 80 CTTTGTGCTCTTGAAGCACCACCAATGGTGGATGCA---AGGTTGCGAGAGACCAAG 136
 Db 78 TTTTGTGCTCTTGAAGCACCACCAATGGTGGAGACACAGAAGTTGGGAGAGCCAAAG 137
 QY 137 TGGGACATGGTACAGGAGTTTGGGAAACCAATGCATGCAGGAACCAATGCAGAAACCT 196
 Db 138 TGGGACATGGTACAGGAGTTTGGGAAACCAATGCATGCAGGAATGCATGAATTAACCT 197
 QY 197 TGAAGACAGAACACAGGATCTTGGCAATATGCTTCCAGCTCACAATGTATTGTGTTA 256
 Db 198 TGAAGACAGAACACATGATCTTGGCAATATGCTTCCAGCTCACAATGTATTGTGTTA 257
 QY 257 CTTCCCATGTTAA 269
 Db 258 CTTCCCATGTTAA 270
 RESULT 12
 CD834090
 LOCUS
 DEFINITION
 BN45.040121F011018 BN45 Brassica napus cDNA clone BN45040121, mRNA sequence.
 ACCESSION
 CD834090
 VERSION
 CD834090.1 GI:32516030
 KEYWORDS
 EST.
 SOURCE
 Brassica napus (rape)
 Brassica napus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica. 1 (bases 1 to 409)
 Genoplante.
 Genoplante, a major partnership french program in plant genomics
 Unpublished (2003)
 Contact: Genoplante
 Genoplante
 93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'genoplante' (<http://www.genoplante.com>)
and <http://genoplante-info.infobiogen.fr>.

Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (<http://www.genoplante.com>
and <http://genoplante-info.infobiogen.fr>).

FEATURES

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1. .409
  /organism="Brassica napus"
  /mol_type="mRNA"
  /culturvar="Jet neuf"
  /db_xref="taxon:3708"
  /clone="BN45040121"
  /tissue_type="seed"
  /clone_lib="BN45"
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ORIGIN

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Query Match      61.6%; Score 176.2; DB 14; Length 409;
Best Local Similarity 83.8%; Pred. No. 1.6e-37;
Matches 212; Conservative 0; Mismatches 38; Indels 3; Gaps 1;

```

QY 20 AGTAATAGATATGGCTAAGTTTGCTACCAATCACTCTCTCTCTTTGGTCGCTTGTCT 79
10 TCTTCTTCAAGCTGGCTTAAAGTTTGTCTTCATCTGCCACATCTTTGCTGCTCTTGTCT 78
10 TCTTCTTCAAGCTGGCTTAAAGTTTGTCTTCATCTGCCACATCTTTGCTGCTCTTGTCT 78

[illegible]

Db	79	TTTCGTGCTTTTCGAAGCACCAACATGGTGGAAAGCACAGAACTTTGTGCGAGAGGCCAAG	138
Qy	137	TGGGACATGGTGTGGAGTTTGTGGGACCAACATGCTGCAGAAACCAATTCGAAACCT	196

db	139	TGGGACATGGTCAGGAGTCTCGGAAACAATAACGCATCGAAGAAATCAGTGCATTAACT	198
	107	TCAAGGCGCAGACACGGATCTTTCGAATCTATGTCCTCCAGCTCACAAATGATTTGTTA	256

Qy
Db

197 TGAAGACGACGATCACCGA |||||
198 TGAAGACGACGATCACCGA |||||
199 TGAGAAGCAGCATGGATCTTGCAATGTCTCCAGCTCACAGTGAATTGCTA 258

Qy 257 CTTCCCATGTTAA 269
|||||
Db 259 CTTCCCTGTTAA 271

RESULT 13

	EST 10-JUL-2000
CD833944	linear mRNA 420 bp
LOCUS	Brassic napus cdna clone BN45040B07, mRNA
CD833944	BN45.040B07F011019, BN45 Brassica napus
DEFINITION	sequence.

ACCESSION CD833944
VERSION CD833944.1
KEYWORDS EST. 1999-1999 (2000) GI: 32515884

SOURCE	
Brassica napus (rape)	
Brassica napus	
ORGANISM	
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Magnoliophyta; eudicotyledons; core eudicots; Gymnosperms; Pinophyta; Pinaceae; Pinus	

REFERENCE
1 (bases 1 to 420)
AUTHORS
Genoplante.
Spermatophytes; magnoliids; rosids; eucosids II; Brassicales; Brassicaceae; Brassica.

Genoplate, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplate

Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10

Fax: 33 1 69 47 54 60
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (<http://www.genoplante.com>
and <http://genoplante-info.infobiogen.fr>).

FEATURES

1. .420
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
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/clone="BN45040H07"

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/tissue_type="seed"  
/clone_lib="BN45"
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Matches	212;	Conservative	0;	Mismatches	38;	Indels	3;	Gaps	1
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40	ACTACTGATCATGGCTAAGTTTGCTTCCATCATTTGCCTACTCTTTTGTCTGCTTTGCTCT	Dδ
80	CTTTTGTGTCCTTTTGAAGCACCACCAACAATGGTGGATGCA--AGGTTGTGCGAGACACCAAG	Dγ

80	CCTGTCCTCGAAGCACACAGAATGTGTGGAGCCCAAG	159
Dd	TTTGGTCTCTCGAAGCACACAAATGGTGAACCATGCAGAACT	196

137 TGGGACATGGTCAGGAGTTTGTGGGAACCAATGCAATGCAAGCAACCAATGCAAGAACCT 139

160 TGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGATCAAGTGCATTAACT 219

[illegible]

DG
229
CGTCCATGGTTAA
QY
257 CTTCCCATTGTAA
269

Db 280 CTTCCCTTGTTAA 292

RESULT	14
CD826491	
LOCUS	linear
DEFINITION	EST 10-JUL-2001
FEATURES	
CDS	421 bp mRNA
ORIGIN	B25_064A05F020416 BN25 Brassica napus cDNA clone BN25064A05, WENA

DEFINITION	
BRZ30800	sequence.
ACCESSION	CD826491
VERSION	CD826491.1 GI:32508431

EST.
KEYWORDS
SOURCE
ORGANISM

REFERENCE
1 (bases 1 to 421)
rosids; eucosids II; Brassicales; Brassicaceae; Brassica.
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Eukaryota; Viridiplantae; Streptophyta.

REFERENCE
AUTHORS
TITLE
JOURNAL
Unpublished (2003)
Genopante, a major partnership french program in plant genomics
Genopante, a major partnership french program in plant genomics
Unpublished (2003)

COMMENT
Contact: Genoplante Genoplante 93, rue Henri Rochefort 91025 EVRY CEDEX France tel. 1 39 47 54 00

Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (<http://www.Genoplante.com>)

FEATURES
 source
 1. 421
 Location/Qualifiers
 and <http://genoplante-info.infobiogen.fr>.
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/organism="Brassica napus"
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ORIGIN	Query Match	Score	DB	Length
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Best Local Similarity 83.8%; Pred. No. 1.6e-37;
Matches 212; Conservative 38; Indels 3; Gaps 79

Qy

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Dβ

41 ACTAGTGATCATGGCTAAAGTTGGCTTCCATCATGCCCTACTCTTTTGGCTGCTCTTGTCTCT 10

Search completed: May 18, 2004, 19:00:29
Job time : 2384.6 secs

FEATURES	source	Location/Qualifiers	and help	ORIGIN
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		/db_xref="taxon:3708"		
		/clone="BN40058A09"		
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		/clone_lib="BN40"		

ORIGIN	Query Match	61.6%;	Score 176.2;	DB 14;	Length 421;
	Best Local Similarity	83.8%;	Pred. No. 1.6e-37;		
	Matches 212;	Conservative	0;	Mismatches 38;	Indels 3; Gaps 1
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DB	41	ACTAGTGATCATGGCTAAGTTTGCTTCCATCATTCGCCCTACTTTTGTCTCTTGTCTT	100		
QY	80	CTTTGCTGCTTTTGAAGCACCAACAATGGTGGATGCA--AGTTGTGCGAGAGCCAAAG	136		
DB	101	TTTTCGCTGCTCTCGAAGCACCAACAATGGTGGAAAGCAGAGAAGTTGTGCGAGAGCCAAAG	160		
QY	137	TGGGCATGGTCAGCAGATTGTGGGACCAACAATGCATGCAGGACCAATGCAGAAAACCT	196		
DB	161	TGGGCATGGTCAGCAGTCTGTGGAAACAATAACCGATGCAAGAATCAGTCGATTAACT	220		
QY	197	TGAAAGAGCAGAACACGGATCTTTGCAACTATGTCTTCCAGCTCCAAATGTATTGTGTA	256		
DB	221	TGAAAGATACGTCATGCGATCTTTGCAACTATGTCTTCCAGCTCCAAATGTATTGTGTA	280		

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 18, 2004, 16:14:01 ; Search time 757.05 Seconds
(without alignments)
8616.891 Million cell updates/sec

Title: US-10-681-972-12_COPY_116_269

Perfect score: 154

Sequence: 1 aagttgtggagagacaa.....tttgttacttcccatgttaa 154

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb.ba.*

2: gb.htg.*

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5: gb.ov.*

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7: gb.ph.*

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31: em.htg.inv.*

32: em.htg.other.*

33: em.htg.mus.*

34: em.htg.pln.*

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37: em.htg.vrt.*

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39: em.htgo.hum.*

40: em.htgo.mus.*

41: em.htgo.other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	154	100.0	270	6	AR014691	Sequence
2	154	100.0	270	6	AR432391	Sequence
3	154	100.0	286	6	AR014689	Sequence
4	154	100.0	286	6	AR432389	Sequence
5	140.2	91.0	500	6	AR014686	Sequence
6	140.2	91.0	500	6	AR432386	Sequence
7	122.6	79.6	526	11	BV010709	MASC_STS1
8	122.6	79.6	574	11	BV010696	MASC_STS1
9	122.6	79.6	575	11	BV010710	MASC_STS1
10	122.6	79.6	578	11	BV010700	MASC_STS1
11	122.6	79.6	602	11	BV010703	MASC_STS1
12	122.6	79.6	61290	8	AB017065	Arabidops
13	122.6	79.6	87080	8	AC004747	Arabidops
14	121	78.6	580	11	BV010699	MASC_STS1
15	121	78.6	582	11	BV010698	MASC_STS1
16	121	78.6	595	11	BV010707	MASC_STS1
17	121	78.6	604	11	BV010711	MASC_STS1
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19	119.4	77.5	243	6	AX412601	Sequence
20	119.4	77.5	243	6	AX651878	Sequence
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22	119.4	77.5	403	6	A68645	Sequence 13
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25	119.4	77.5	497	11	BV010712	MASC_STS1
26	119.4	77.5	541	11	BV010697	MASC_STS1
27	119.4	77.5	563	11	BV010667	MASC_STS1
28	119.4	77.5	572	11	BV010673	MASC_STS1
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32	117.8	76.5	243	6	AX412329	Sequence
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34	117.8	76.5	243	6	AX507351	Sequence
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36	117.8	76.5	243	6	BD174927	Disease t
37	117.8	76.5	274	8	AY133787	Arabidops
38	117.8	76.5	395	8	RSU18557	Raphanus sa
39	117.8	76.5	400	6	A68647	Sequence 15
40	117.8	76.5	414	6	A26875	R.sativus A
41	117.8	76.5	414	6	A39549	Sequence 37
42	117.8	76.5	414	6	A63404	Sequence 19
43	117.8	76.5	414	6	AR050153	Sequence
44	117.8	76.5	414	6	AR130272	Sequence
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ALIGNMENTS

RESULT 1
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LOCUS AR014691 270 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 14 from patent US 5773696.
ACCESSION AR014691
VERSION AR014691.1 GI:3972145
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 270)
AUTHORS Liang,J., Shah,D.Maganlal., Wu,Y.Shun. and Rosenberger,C.Annette..
TITLE Antifungal polypeptide and methods for controlling plant pathogenic fungi
JOURNAL Patent: US 5773696-A 14 30-JUN-1998;

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Db 108 AAGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATG 167
QY 61 CAGGAACCAATGCAGAACCTTGAAGAGCAGACACCGATCTTGCACATATGTCTTCCC 120
    |||
Db 168 CAGGAACCAATGCAGAACCTTGAAGAGCAGACACCGATCTTGCACATATGTCTTCCC 227
QY 121 AGCTCACAATGTATTGTTGTTACTTCCCATGTTAA 154
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Db 228 AGCTCACAATGTATTGTTGTTACTTCCCATGTTAA 261

RESULT 2
LOCUS               AR432391                270 bp DNA linear PAT 18-DEC-2003
DEFINITION          Sequence 14 from patent US 6653280.
ACCESSION            AR432391
VERSION              AR432391.1 GI:40194668
KEYWORDS             Unknown.
SOURCE               Unknown.
ORGANISM             Unclassified.
REFERENCE            1 (bases 1 to 270)
AUTHORS              Liang,J., Shah,D.M., Wu,Y.S. and Rosenberger,C.A.
TITLE               Antifungal polypeptide AlyAPP from Alyssum and methods for
controlling plant pathogenic fungi
Patent: US 6653280-A 14 25-NOV-2003;
JOURNAL              Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 3.8e-36;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 108 AAGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATG 167
QY 61 CAGGAACCAATGCAGAACCTTGAAGAGCAGACACCGATCTTGCACATATGTCTTCCC 120
    |||
Db 168 CAGGAACCAATGCAGAACCTTGAAGAGCAGACACCGATCTTGCACATATGTCTTCCC 227
QY 121 AGCTCACAATGTATTGTTGTTACTTCCCATGTTAA 154
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Db 228 AGCTCACAATGTATTGTTGTTACTTCCCATGTTAA 261

RESULT 3
LOCUS               AR014689                286 bp DNA linear PAT 05-DEC-1998
DEFINITION          Sequence 12 from patent US 5773696.
ACCESSION            AR014689
VERSION              AR014689.1 GI:3972143
KEYWORDS             Unknown.
SOURCE               Unknown.
ORGANISM             Unclassified.
REFERENCE            1 (bases 1 to 286)
AUTHORS              Liang,J., Shah,D.M., Wu,Y.S. and Rosenberger,C.A.
TITLE               Antifungal polypeptide AlyAPP from Alyssum and methods for
controlling plant pathogenic fungi
Patent: US 5773696-A 12 25-NOV-2003;
JOURNAL              Location/Qualifiers
FEATURES             1..286
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Best Local Similarity 100.0%; Pred. No. 3.8e-36;
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QY 61 CAGGAACCAATGCAGAACCTTGAAGAGCAGACACCGATCTTGCACATATGTCTTCCC 120
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Db 176 CAGGAACCAATGCAGAACCTTGAAGAGCAGACACCGATCTTGCACATATGTCTTCCC 235
QY 121 AGCTCACAATGTATTGTTGTTACTTCCCATGTTAA 154
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Db 236 AGCTCACAATGTATTGTTGTTACTTCCCATGTTAA 269

RESULT 4
LOCUS               AR432389                286 bp DNA linear PAT 18-DEC-2003
DEFINITION          Sequence 12 from patent US 6653280.
ACCESSION            AR432389
VERSION              AR432389.1 GI:40194666
KEYWORDS             Unknown.
SOURCE               Unknown.
ORGANISM             Unclassified.
REFERENCE            1 (bases 1 to 286)
AUTHORS              Liang,J., Shah,D.M., Wu,Y.S. and Rosenberger,C.A.
TITLE               Antifungal polypeptide AlyAPP from Alyssum and methods for
controlling plant pathogenic fungi
Patent: US 6653280-A 12 25-NOV-2003;
JOURNAL              Location/Qualifiers
FEATURES             1..286
source              /organism="unknown"
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Best Local Similarity 100.0%; Pred. No. 3.8e-36;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 CAGGAACCAATGCAGAACCTTGAAGAGCAGACACCGATCTTGCACATATGTCTTCCC 120
    |||
Db 176 CAGGAACCAATGCAGAACCTTGAAGAGCAGACACCGATCTTGCACATATGTCTTCCC 235
QY 121 AGCTCACAATGTATTGTTGTTACTTCCCATGTTAA 154
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Db 236 AGCTCACAATGTATTGTTGTTACTTCCCATGTTAA 269

RESULT 5
LOCUS               AR014686                500 bp DNA linear PAT 05-DEC-1998
DEFINITION          Sequence 9 from patent US 5773696.
ACCESSION            AR014686
VERSION              AR014686.1 GI:3972140
KEYWORDS             Unknown.
SOURCE               Unknown.
ORGANISM             Unknown.

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TITLE               Antifungal polypeptide and methods for controlling plant pathogenic
fungi
JOURNAL             Patent: US 5773696-A 12 30-JUN-1998;
FEATURES             Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 3.8e-36;
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Db 116 AAGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATG 175
QY 61 CAGGAACCAATGCAGAACCTTGAAGAGCAGACACCGATCTTGCACATATGTCTTCCC 120
    |||
Db 176 CAGGAACCAATGCAGAACCTTGAAGAGCAGACACCGATCTTGCACATATGTCTTCCC 235
QY 121 AGCTCACAATGTATTGTTGTTACTTCCCATGTTAA 154
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Db 236 AGCTCACAATGTATTGTTGTTACTTCCCATGTTAA 269

RESULT 4
LOCUS               AR432389                286 bp DNA linear PAT 18-DEC-2003
DEFINITION          Sequence 12 from patent US 6653280.
ACCESSION            AR432389
VERSION              AR432389.1 GI:40194666
KEYWORDS             Unknown.
SOURCE               Unknown.
ORGANISM             Unclassified.
REFERENCE            1 (bases 1 to 286)
AUTHORS              Liang,J., Shah,D.M., Wu,Y.S. and Rosenberger,C.A.
TITLE               Antifungal polypeptide AlyAPP from Alyssum and methods for
controlling plant pathogenic fungi
Patent: US 6653280-A 12 25-NOV-2003;
JOURNAL              Location/Qualifiers
FEATURES             1..286
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Db 116 AAGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATG 175
QY 61 CAGGAACCAATGCAGAACCTTGAAGAGCAGACACCGATCTTGCACATATGTCTTCCC 120
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Db 176 CAGGAACCAATGCAGAACCTTGAAGAGCAGACACCGATCTTGCACATATGTCTTCCC 235
QY 121 AGCTCACAATGTATTGTTGTTACTTCCCATGTTAA 154
    |||
Db 236 AGCTCACAATGTATTGTTGTTACTTCCCATGTTAA 269

RESULT 5
LOCUS               AR014686                500 bp DNA linear PAT 05-DEC-1998
DEFINITION          Sequence 9 from patent US 5773696.
ACCESSION            AR014686
VERSION              AR014686.1 GI:3972140
KEYWORDS             Unknown.
SOURCE               Unknown.
ORGANISM             Unknown.

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Unclassified.
REFERENCE 1 (bases 1 to 500)
AUTHORS Liang,J., Shah,D.Maganlal., Wu,Y.Shun. and Rosenberger,C.Annette.
TITLE Antifungal polypeptide and methods for controlling plant pathogenic
JOURNAL fungi
FEATURES Patent: US 5773696-A 9 30-JUN-1998;
source Location/Qualifiers
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159 AAGTTGTGCGAGAGTCCAGTGGAAATGTCAGCGGTGTGGGAATAATAACGATGC 218
QY 62 AGGAACCAATGCAGAAACCTTGAAGAGCAGAACACGGATCTTGCAACTATGCTTCCCA 121
Db |||||||
219 AGGAACCAATGCAGAAACCTTGAAGAGCAGAACACGGATCTTGCAACTATGCTTCCCA 278
QY 122 GCTCACAATGATTTGTTACTTCCCATGTTAA 154
Db |||||||
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RESULT 6
LOCUS AR432386 500 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 9 from patent US 6653280.
ACCESSION AR432386
VERSION AR432386.1 GI:40194663
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 500)
AUTHORS Liang,J., Shah,D.M., Wu,Y.S. and Rosenberger,C.A.
TITLE Antifungal polypeptide AlyAFP from Alysum and methods for
controlling plant pathogenic fungi
JOURNAL Patent: US 6653280-A 9 25-NOV-2003;
FEATURES Location/Qualifiers
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Best Local Similarity 94.8%; Pred. No. 6.1e-32;
Matches 145; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Db |||||||
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Db |||||||
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RESULT 7
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DEFINITION MASC STS16442 Arabidopsis thaliana (Landsberg erecta accession)
GENOMIC DNA Arabidopsis thaliana STS genomic, sequence tagged site.
ACCESSION BV010709

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VERSION BV010709.1 GI:32963207
KEYWORDS STS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 526)
AUTHORS Schmid,K.J., Sorensen,T.R., Stracke,R., Torjek,O., Altmann,T.,
Mitchell-Olds,T. and Weisshaar,B.
TITLE Large-Scale Identification and Analysis of Genome-Wide
Single-Nucleotide Polymorphisms for Mapping in Arabidopsis thaliana
JOURNAL Genome Res. 13 (6), 1250-1257 (2003)
MEDLINE 22683290
PubMed 12799357
COMMENT Synonyms: PCP16C2 ler.a
Contact: Karl Schmid
Department of Genetics and Evolution
Max-Planck-Institute of Chemical Ecology
Winzerlaer Str. 10, 07745 Jena, Germany
Tel: + 49-3641-571465
Fax: + 49-3641-571402
Email: schmid@ice.mpg.de
Primer A: CGCTGCTCTGTTCTCTTTG
Primer B: AAACAAACCGTTGTTGGTCA
STS size: 526
PCR Profile:
Presoak: 94 degrees for 2.00 minute(s)
Denaturation: 94 degrees for 0.50 minute(s)
Annealing: 58 degrees for 0.50 minute(s)
Polymerization: 72 degrees for 1.00 minute(s)
PCR Cycles: 35
Thermal Cycler: Perkin Elmer GeneAmp9600
Protocol:
Template: 20 - 100 ng
Primer: each 1 uM
dNTPs: each 400 uM
Taq Polymerase: 0.05 units/uL
Total Vol: 10 uL
Buffer:
MgCl2: 1.5 mM
KCl: 50 mM
Tris-HCl: 10 mM
pH: 8.3.
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assembled into a consensus sequence. Note: Sequencing
granted in the context of the GABI Arabidopsis Verbund:
Genetic Diversity, 'Establishment of high-efficiency
SNP-based mapping tools and development of methods for
genome-wide mutation detection' PIs: Thomas Altmann,
Thomas Mitchell-Olds, Bernd Weisshaar"
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Best Local Similarity 87.6%; Pred. No. 1.4e-26;
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 2 AGTTTGTGCGAGAGACCAAGTGGACATGTCAGAGTTTGGGAACAACATGATGC 61
Db |||||||
42 AAGTTTGTGCGAGAGACCAAGTGGATGTCAGAGTTTGGGAACAACATGATGC 101
QY 62 AGGAACCAATGCAGAAACCTTGAAGAGCAGAACACGGATCTTGCAACTATGCTTCCCA 121

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Db 102 AAGAATCAGTGCAATTAACCTTGAAGAGCAAAACATGGAATCTTGCACACTATGTCTTCCCA 161
 QY 122 GCTCACAAGTATTTCTTACTTCCCATGTAA 154
 Db 162 GCTCACAAGTATTTCTTACTTCCCATGTAA 194

RESULT 8
 BV010696/c
 LOCUS 574 bp DNA linear STS 18-JUL-2003
 DEFINITION MASC_ST516441 Arabidopsis thaliana (Eifel-2 accession) genomic DNA
 Arabidopsis thaliana STS genomic, sequence tagged site.

ACCESSION BV010696
 VERSION BV010696.1 GI:32963194
 KEYWORDS STS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 574)

AUTHORS Schmid,K.J., Sorensen,T.R., Stracke,R., Torjek,O., Altmann,T.,

Mitchell-Olds,T. and Weisshaar,B.

TITLE Large-Scale Identification and Analysis of Genome-Wide
 Single-Nucleotide Polymorphisms for Mapping in Arabidopsis thaliana

JOURNAL Genome Res. 13 (6), 1250-1257 (2003)

MEDLINE 22683290

PUBMED 12799357

COMMENT Synonyms: PCP16C2.ei2.a

Contact: Karl Schmid

Department of Genetics and Evolution

Max-Planck-Institute of Chemical Ecology

Winzerlaer Str. 10, 07745 Jena, Germany

Tel: + 49-3641-571465

Fax: + 49-3641-571402

Email: schmid@ice.mpg.de

Primer A: CGCTGCTCTTGTCTCTTTTG

Primer B: AAACAACCGTTGTTGGTCA

STS size: 574

PCR Profile:

Presoak: 94 degrees for 2.00 minute(s)

Denaturation: 94 degrees for 0.50 minute(s)

Annealing: 58 degrees for 0.50 minute(s)

Polymerization: 72 degrees for 1.00 minute(s)

PCR Cycles: 35

Thermal Cycler: Perkin Elmer GeneAmp9600

Protocol:

Template: 20 - 100 ng

Primer: each 1 uM

dNTPs: each 400 uM

Taq Polymerase: 0.05 units/ul

Total Vol: 10 ul

Buffer:

MgCl2: 1.5 mM

KCl: 50 mM

Tris-HCl: 10 mM

pH: 8.3.

FEATURES

Source

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/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/strain="Eifel-2"

/db_xref="taxon:3702"

/clone_lib="Arabidopsis thaliana (Eifel-2 accession)

genomic DNA"

/note="Genomic DNA prepared from rosette leaves. DNA was

amplified and directly sequenced from both directions and

assembled into a consensus sequence. Note: Sequencing

granted in the context of the GABI Arabidopsis Verbund:

Genetic Diversity, 'Establishment of high-efficiency

SNP-based mapping tools and development of methods for

genome-wide mutation detection' PIs: Thomas Altmann,
 Thomas Mitchell-Olds, Bernd Weisshaar"

<1..574

ORIGIN

Query Match

Best Local Similarity 79.6%; Score 122.6; DB 11; Length 574;

Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 2 AGTTGTGCGAGAGACCAAGTGGACATGTCAGGAGTTTGTGCGAACCAACATGTCATGC 61

Db 486 AAGTTGTGCGAGAGCAAGTGGTACTTGTGTCAGGAGTTTGTGCGAACCAACATGTCATGC 427

QY 62 AGCAACCAATGCGAAGAACCTTGAAGAGCAGACACGGATCTTGGCACTATGTCCTCCCA 121

Db 426 AAGAATCAGTGCATTAACTTGAAGAGCAGACACATGGATCTTGGCACTATGTCCTCCCA 367

QY 122 GCTCACAAGTATTTCTTACTTCCCATGTAA 154

Db 366 GCTCACAAGTATTTCTTACTTCCCATGTAA 334

RESULT 9

BV010710

LOCUS 575 bp DNA linear STS 18-JUL-2003

DEFINITION MASC_ST516443 Arabidopsis thaliana (Weinlingen-0 accession) genomic

DNA Arabidopsis thaliana STS genomic, sequence tagged site.

ACCESSION BV010710

VERSION BV010710.1 GI:32963208

KEYWORDS STS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 575)

AUTHORS Schmid,K.J., Sorensen,T.R., Stracke,R., Torjek,O., Altmann,T.,

Mitchell-Olds,T. and Weisshaar,B.

TITLE Large-Scale Identification and Analysis of Genome-Wide

Single-Nucleotide Polymorphisms for Mapping in Arabidopsis thaliana

JOURNAL Genome Res. 13 (6), 1250-1257 (2003)

MEDLINE 22683290

PUBMED 12799357

COMMENT Synonyms: PCP16C2.wei0.a

Contact: Karl Schmid

Department of Genetics and Evolution

Max-Planck-Institute of Chemical Ecology

Winzerlaer Str. 10, 07745 Jena, Germany

Tel: + 49-3641-571465

Fax: + 49-3641-571402

Email: schmid@ice.mpg.de

Primer A: CGCTGCTCTTGTCTCTTTTG

Primer B: AAACAACCGTTGTTGGTCA

STS size: 575

PCR Profile:

Presoak: 94 degrees for 2.00 minute(s)

Denaturation: 94 degrees for 0.50 minute(s)

Annealing: 58 degrees for 0.50 minute(s)

Polymerization: 72 degrees for 1.00 minute(s)

PCR Cycles: 35

Thermal Cycler: Perkin Elmer GeneAmp9600

Protocol:

Template: 20 - 100 ng

Primer: each 1 uM

dNTPs: each 400 uM

Taq Polymerase: 0.05 units/ul

Total Vol: 10 ul

Buffer:

MgCl2: 1.5 mM

KCl: 50 mM

Tris-HCl: 10 mM

pH: 8.3.

Protocol:

Template: 20 - 100 ng

Primer: each 1 uM

dNTPs: each 400 uM

Taq Polymerase: 0.05 units/ul

Total Vol: 10 ul

Buffer:

MgCl2: 1.5 mM

KCl: 50 mM

Tris-HCl: 10 mM

pH: 8.3.

FEATURES

source
 Location/Qualifiers
 1. .575
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 /mol_type="genomic DNA"
 /strain="Weinlingen-0"
 /db_xref="taxon:3702"
 /clone_lib="Arabidopsis thaliana (Weinlingen-0 accession)
 genomic DNA"
 /notes="Genomic DNA prepared from rosette leaves. DNA was amplified and directly sequenced from both directions and assembled into a consensus sequence. Note: Sequencing granted in the context of the GABI Arabidopsis Verbund: Genetic Diversity, 'Establishment of high-efficiency SNP-based mapping tools and development of methods for genome-wide mutation detection' PIs: Thomas Altmann, Thomas Mitchell-Olds, Bernd Weisshaar"
 <1. .575

STS
ORIGIN

Query Match 79.6%; Score 122.6; DB 11; Length 575;
 Best Local Similarity 87.6%; Pred. No. 1.4e-26;
 Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
 QY 2 AGTTGTGCGAGAGACCAAGTGGACATGTCAGGAGTTGTGGGAACAATGCATGC 61
 Db |||||
 92 AAGTTGTGCGAGAGACCAAGTGGTACTGTGTCAGGAGTTGTGGGAACAATGCATGC 151
 QY 62 AGGAACCAATGCAGAACCTTGAAGAGCAGAACACGGATCTTGCACACTATGCTTCCCA 121
 Db |||||
 152 AAGAATCAGTGCATTAACCTTGAAGAGCAGAACACATGATCTTGCACACTATGCTTCCCA 211
 QY 122 GCTCACAATGTATTTGTTACTTCCCATGTTAA 154
 Db |||||
 212 GCTCACAAGTATCTGTTAGTCCCATGTTAA 244

RESULT 10
BV010700/c

LOCUS 578 bp DNA linear STS 18-JUL-2003
 DEFINITION MASC STS16437 Arabidopsis thaliana (Lezoux/Puy-de-Dome-0 accession)
 genomic DNA Arabidopsis thaliana STS genomic, sequence tagged site.
 ACCESSION BV010700
 VERSION 1 GI:32963198
 KEYWORDS STS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 1 (bases 1 to 578)
 Schmid,K.J., Sorensen,T.R., Stracke,R., Torjek,O., Altmann,T., Mitchell-Olds,T. and Weisshaar,B.
 Large-Scale Identification and Analysis of Genome-Wide Single-Nucleotide Polymorphisms for Mapping in Arabidopsis thaliana
 Genome Res. 13 (6), 1250-1257 (2003)
 22683290
 12799357
 Synonyms: PCP16C2.1z0.a
 Contact: Karl Schmid
 Department of Genetics and Evolution
 Max-Planck-Institute of Chemical Ecology
 Winzerlaer Str. 10, 07745 Jena, Germany
 Tel: + 49-3641-571465
 Fax: + 49-3641-571402
 Email: schmid@ice.mpg.de
 Primer A: CGCTGCTCTGTCTCTCTTTG
 Primer B: AAACAACCGTGTGTGGTCA
 STS size: 578
 PCR Profile:
 Presoak: 94 degrees for 2.00 minute(s)
 Denaturation: 94 degrees for 0.50 minute(s)
 Annealing: 58 degrees for 0.50 minute(s)
 Polymerization: 72 degrees for 1.00 minute(s)

PCR Cycles: 35

Thermal Cycler: Perkin Elmer GeneAmp9600

Protocol:

Template: 20 - 100 ng
 each 1 uM
 Primers: each 400 uM
 dNTPs: each 400 uM
 Tag Polymerase: 0.05 units/uL
 Total Vol: 10 uL

Buffer:

MgCl2: 1.5 mM
 KCl: 50 mM
 Tris-HCl: 10 mM
 pH: 8.3.

Location/Qualifiers

1. .578
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Lezoux/Puy-de-Dome-0"
 /db_xref="taxon:3702"
 /clone_lib="Arabidopsis thaliana (Lezoux/Puy-de-Dome-0 accession) genomic DNA"

/notes="Genomic DNA prepared from rosette leaves. DNA was amplified and directly sequenced from both directions and assembled into a consensus sequence. Note: Sequencing granted in the context of the GABI Arabidopsis Verbund: Genetic Diversity, 'Establishment of high-efficiency SNP-based mapping tools and development of methods for genome-wide mutation detection' PIs: Thomas Altmann, Thomas Mitchell-Olds, Bernd Weisshaar"
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FEATURES
sourceSTS
ORIGIN

Query Match 79.6%; Score 122.6; DB 11; Length 578;
 Best Local Similarity 87.6%; Pred. No. 1.4e-26;
 Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
 QY 2 AGTTGTGCGAGAGACCAAGTGGACATGTCAGGAGTTGTGGGAACAATGCATGC 61
 Db |||||
 486 AAGTTGTGCGAGAGACCAAGTGGTACTGTGTCAGGAGTTGTGGGAACAATGCATGC 427
 QY 62 AGGAACCAATGCAGAACCTTGAAGAGCAGAACACGGATCTTGCACACTATGCTTCCCA 121
 Db |||||
 426 AAGAATCAGTGCATTAACCTTGAAGAGCAGAACACATGATCTTGCACACTATGCTTCCCA 367
 QY 122 GCTCACAATGTATTTGTTACTTCCCATGTTAA 154
 Db |||||
 366 GCTCACAAGTATCTGTTAGTCCCATGTTAA 334

RESULT 11
BV010703/c

LOCUS 602 bp DNA linear STS 18-JUL-2003
 DEFINITION MASC STS16436 Arabidopsis thaliana (Gueckingen-0 accession) genomic
 DNA Arabidopsis thaliana STS genomic, sequence tagged site.
 ACCESSION BV010703
 VERSION 1 GI:32963201
 KEYWORDS STS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 1 (bases 1 to 602)
 Schmid,K.J., Sorensen,T.R., Stracke,R., Torjek,O., Altmann,T., Mitchell-Olds,T. and Weisshaar,B.
 Large-Scale Identification and Analysis of Genome-Wide Single-Nucleotide Polymorphisms for Mapping in Arabidopsis thaliana
 Genome Res. 13 (6), 1250-1257 (2003)
 22683290
 12799357
 Synonyms: PCP16C2.gue0.a
 Contact: Karl Schmid

Department of Genetics and Evolution
 Max-Planck-Institute of Chemical Ecology
 Winzlerlaer Str. 10, 07745 Jena, Germany
 Tel: + 49-3641-571465
 Fax: + 49-3641-571402
 Email: schmid@ice.mpg.de
 Primer A: CGTGTCTCTGTCCTCTTG
 Primer B: AACCAACCGTGTGTGTC
 STS size: 602
 PCR Profile:

Presoak: 94 degrees for 2.00 minute(s)
 Denaturation: 94 degrees for 0.50 minute(s)
 Annealing: 58 degrees for 0.50 minute(s)
 Polymerization: 72 degrees for 1.00 minute(s)
 PCR Cycles: 35
 Thermal Cycler: Perkin Elmer GeneAmp9600
 Protocol:
 Template: 20 - 100 ng
 Primer: each 1 uM
 dNTPs: each 400 uM
 Taq Polymerase: 0.05 units/ul
 Total Vol: 10 ul

Buffer:
 MgCl2: 1.5 mM
 KCl: 50 mM
 Tris-HCl: 10 mM
 pH: 8.3.

FEATURES

source
 Location/Qualifiers
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 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Gueckingen-0"
 /db_xref="taxon:3702"
 /clone_lib="Arabidopsis thaliana (Gueckingen-0 accession)
 /note="Genomic DNA prepared from rosette leaves. DNA was amplified and directly sequenced from both directions and assembled into a consensus sequence. Note: Sequencing granted in the context of the GABI Arabidopsis Verbund I: Genetic diversity, 'Establishment of high-efficiency SNP-based mapping tools and development of methods for genome-wide mutation detection' PIS: Thomas Altmann, Thomas Mitchell-Olds, Bernd Weisshaar"
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STS

ORIGIN

Query Match 79.8%; Score 122.6; DB 11; Length 602;
 Best Local Similarity 87.6%; Pred. No. 1.4e-26;
 Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
 QY 2 AGTTGTGGAGACCAAGTGGACATGTCAGGAGTTGTGGGAACACATGATGC 61
 Db |||||
 509 AGTTGTGGAGAACCAAGTGGATCTTGTGAGGATTTGCGAACAACGATGATGC 450
 QY 62 AGCAACCAATGCAGAAACCTTGAAGAGCAGACACGATCTTGCACACTATGCTTCCCA 121
 Db |||||
 449 AAGAATCAGTGCAATTAACCTTGAAGAGCAACATGATCTTGCACACTATGCTTCCCA 390
 QY 122 GCTCAAAATGATTTGTTACTTCCCATGTAA 154
 Db |||||
 389 GCTCAAAATGATCTGTTACGTCCTCCATGTAA 357

RESULT 12

AB017065/c 61290 bp DNA linear PLN 27-DEC-2000
 LOCUS Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MFC16.
 DEFINITION Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MFC16.
 ACCESSION AB017065 BA000015
 VERSION AB017065.1 GI:3510341
 KEYWORDS Arabidopsis thaliana (thale cress)
 SOURCE Arabidopsis thaliana
 ORGANISM Arabidopsis thaliana

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 1 (sites)
 Kaneko,T., Katoh,T., Sato,S., Nakamura,Y., Asamizu,E., Kotani,H.,
 Miyajima,N. and Tabata,S.
 Structural analysis of Arabidopsis thaliana chromosome 5. IX.
 Sequence features of the regions of 1,011,550 bp covered by
 seventeen P1 and TAC clones
 DNA Res. 6 (3), 183-195 (1999)

REFERENCE

AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL

1 (bases 1 to 61290)

Direct Submission

Submitted (26-AUG-1998) Yasukazu Nakamura, Kazusa DNA Research
 Institute, Department of Plant Gene Research; 1532-3, Yana,
 Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp,
 Tel:81-438-52-3935, Fax:81-438-52-3934)

Address for correspondence: kaos@kazusa.or.jp

For the latest information on annotation of this clone, please see
 http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MFC16
 Genes with similarity to proteins in the databases are described in
 'product' or 'note' qualifiers. Genes that have no significant
 protein similarity are described as 'unknown protein'.

The software programs used to predict genes include: Grail
 (Informatics Group, Oak Ridge National Laboratory,
 http://compbio.ornl.gov/Grail-1.3/),

GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
 NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
 Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
 SplicePredictor (Volker Brendel, Stanford University,
 http://greenlab.zool.iastate.edu/cgi-bin/sp.cgi).

Genes encoding tRNAs are predicted by tRNAscan-SE

(Sean Eddy, Washington University School of Medicine, St. Louis,
 http://genome.wustl.edu/eddy/tRNAscan-SE/).

This sequence may not be the entire insert of this clone. It may be
 shorter because we remove overlaps between neighboring submissions.
 The 5' clone is K9L2 and the 3' clone is K15C23.

FEATURES

source

1..61290
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 /note="CDS is reported in Acc# AB011475
 gene_id:K9L2.20"
 /number=2
 /evidence=not_experimental
 complement(1020..1516)
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 /note="CDS is reported in Acc# AB011475
 gene_id:K9L2.20"
 /number=1
 /evidence=not_experimental
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 /note="gene_id:MFC16.3"
 /codon_start=1
 /evidence=not_experimental
 /product="berberine bridge enzyme-like protein"
 /protein_id="BAB03147.1"
 /db_xref="GI:9758693"

exon

exon

CDS

SOURCE Arabidopsis thaliana (chale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (bases 1 to 87080)
 AUTHORS Rounsley S.D., Kaul S., Lin X., Ketchum K.A., Crosby, M.L.,
 Brandon, R.C., Sykes, S.M., Mason, T.M., Kerlavage, A.R., Adams, M.D.,
 Somerville, C.R. and Venter, J.C.
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 87080)
 AUTHORS Lin, X.
 TITLE Direct Submission
 JOURNAL Submitted (09-MAR-2000) The Institute for Genomic Research, 9712
 Medical Center Dr., Rockville, MD 20850, USA
 REFERENCE 3 (bases 1 to 87080)
 AUTHORS Town, C.D. and Kaul, S.
 TITLE Direct Submission
 JOURNAL Submitted (27-FEB-2002) The Institute for Genomic Research, 9712
 Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.org
 COMMENT On Apr 18, 2002 this sequence version replaced gi:659844.
 FEATURES
 source
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 /mol_type="genomic DNA"
 /cultivar="Columbia"
 /db_xref="taxon:3702"
 /chromosome="2"
 /map="B68"
 /clone="T19L18"
 /note="overlap with BAC clone T1D16
 (AC004484:75774..82212)."
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 /db_xref="GI:20197265"
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 LVTDIIOGAAGVDFGLSGKPKIKQVEVDFINQHYVSTQLKMDLSGLSILGLLI
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 RESDPAKNIPTSDVTSVTVSEHLAAGSATTAFTLSVLYSGHLDVSKLLQETDG
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 /db_xref="GI:20197267"
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 QLLTPSQQLDLDLAKFEVSEIQRQSYEHIFDKYLIQGVIGKEGSHLSRVVFDNLIF

AVGQDDKIWCKSGESSRIWTIKIKNOVEDFLDIILHKQVYALDLTGAIWWSISPL
 SLLOFTSIPMDYDYSCKRLVEYGDLCIIHQRLKRAYIRRSORTQVFKVYKMD
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 /db_xref="GI:3413699"
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 YGFKIDPDRWEFANEGFLAQKHLNKRNNRNNQNVNQSGNSCVGVQYGF
 GEVRLKRDHGVIAEVVRLRQQHSSQVAAMEQRLVTEKQQQQNMFLAKALNN
 PNFVQPAVMSKSKSLFLGLDVGKRLTSTPSLTMEENLLHQPQFPMKDDMEMLF
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 VDQMGFLGSEP"
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 /note="synonym: T19L18.5; contains similarity to YME1
 GI:295582, a member of the ftsH SEC18 PAS1 CDC48 family of
 putative ATPase encoding genes from (Saccharomyces
 cerevisiae)."
 join(9239..9395,9823..9910,9992..10264,10403..10639,
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 TASAPHTISTERTHFQKQLSTIRTIQVGLFLLISIGALIEDRGLGKGLGHEEVQ
 SNDSSTKFSVKGVDKAELEIEIVHLYRDKPRFTLGLGKLPKVLVGPFGTGM
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 DVTMSDLERAKDRIMKSEKSAVSDSEKLTAEHGGHALVAITHEGALPVHKATI
 VPRGALGVSQLPDKDSTISKQMLAKLDVCMGRVABELIFGESEVTSASSDLE
 QATKLARAVMTKFGSKVEGLVAHNYDNGKSMSTETRLIISEVKQLLEKAYNNAKT
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 17080..>17361))
 /gene="At2g26130"
 complement(join(13028..13137,13438..13642,13658..13791,
 13802..13988,14056..14196,14275..14395,16272..17008,
 17080..17361))
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 /translation="MEEDLNPAKPLVRLYFKGLVTEKEMLLAGFGVAICGDKDDL
 LFDLKVSHDPTITLLEVLIALKGLNOAVSINGINHSICCDHYIFELVMSIPPK
 QRSIALLRDVGIRKYLTSIPVMTQNSLAYDFAIEASSEIIDIIPAKETCN
 ICINDINADQMFSDKSGHMCCECKVHIEVRLLEGSLITICPHYRCNSLITSVRCG
 NLLTPKLNQWQKTKDELIPVMDRVYCPNPRCSITLMSGLNIGVRRCCVCKGGE

[illegible]

Db 153 AAGAATCAGTCATTAACTCTGAGGAGCAAAACATGGATCTTGCAACTATGCTTCCCA 212
 QY 122 GCTCAAAATGATTGTTTACTTCCCATGTTAA 154
 Db 213 GCTCAAAAGTGATCTGTTTACGTCCCATGTTAA 245

RESULT 15

BV010698 582 bp DNA linear STS 18-JUL-2003
 LOCUS MASC STS16439 Arabidopsis thaliana (Konchezero accession) genomic
 DEFINITION DNA Arabidopsis thaliana STS genomic, sequence tagged site.

ACCESSION BV010698
 VERSION BV010698.1 GI:32963196
 KEYWORDS STS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 582)
 AUTHORS Schmidt,K.J., Sorensen,T.R., Stracke,R., Torjek,O., Altmann,T.,
 Mitchell-Olds,T. and Weisshaar,B.
 TITLE Large-Scale Identification and Analysis of Genome-Wide
 Single-Nucleotide Polymorphisms for Mapping in Arabidopsis thaliana
 Genome Res. 13 (6), 1250-1257 (2003)

JOURNAL 22683230
 MEDLINE 12799357
 PUBMED
 COMMENT

Synonyms: PCP16C2_cs22491.a
 Contact: Karl Schmid
 Department of Genetics and Evolution
 Max-Planck-Institute of Chemical Ecology
 Winzerlaer Str. 10, 07745 Jena, Germany
 Tel: + 49-3641-571465
 Fax: + 49-3641-571402
 Email: schmid@ice.mpg.de
 Primer A: CGCTGCTCTGTGTTCTCTTG
 Primer B: AAACAACCGTGTGTTGGTCA
 STS size: 582

PCR Profile:

Presoak: 94 degrees for 2.00 minute(s)
 Denaturation: 94 degrees for 0.50 minute(s)
 Annealing: 58 degrees for 0.50 minute(s)
 Polymerization: 72 degrees for 1.00 minute(s)
 PCR Cycles: 35
 Thermal Cycler: Perkin Elmer GeneAmp9600

Protocol:

Template: 20 - 100 ng
 Primer: each 1 uM
 dNTPs: each 400 uM
 Taq Polymerase: 0.05 units/ul
 Total Vol: 10 ul

Buffer:

MgCl2: 1.5 mM
 KCl: 50 mM
 Tris-HCl: 10 mM
 pH: 8.3

FEATURES
source

Location/Qualifiers
 1..582
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Konchezero"
 /db_xref="taxon:3702"
 /clone_lib="Arabidopsis thaliana (Konchezero accession)
 genomic DNA"
 /note="Genomic DNA prepared from rosette leaves. DNA was
 amplified and directly sequenced from both directions and
 assembled into a consensus sequence. Note: Sequencing
 granted in the context of the GABI Arabidopsis VerbundI:
 Genetic Diversity, 'Establishment of high-efficiency
 SNP-based mapping tools and development of methods for
 genome-wide mutation detection' PIs: Thomas Altmann,

ORIGIN
 Thomas Mitchell-Olds, Bernd Weisshaar"
 <1..>582

Query Match 78.6%; Score 121; DB 11; Length 582;
 Best Local Similarity 86.9%; Pred. No. 4.3e-26;
 Matches 133; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 QY 2 AGTTTGTGGAGAGACCAAGTGGGACATGGTCAGAGTTTGTGGGAACAACAATGCATGC 61
 Db 94 AAGTTGTGGAGAACCCAAAGTGGTACTTGGTCAGAGTTTGGGAACAACAATGCATGC 153
 QY 62 AGGAACCAATGCGAGAAACCTTGAAAAGAGCAGAACACGGATCTTGCAACTATATGCTTCCCA 121
 Db 154 AAGAATCAGTCATTAACTTGAGGGAGACAAACATGGATCTTGCAACTATGCTTCCCA 213
 QY 122 GCTCAAAATGATTGTTGTTACTTCCCATGTTAA 154
 Db 214 GCTCAAAAGTGATCTGTTTACGTCCCATGTTAA 246

Search completed: May 18, 2004, 17:59:04
 Job time : 758.05 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 18, 2004, 16:12:26 ; Search time 150.15 Seconds

(without alignments)
4357.126 Million cell updates/sec

Title: US-10-681-972-12_COPY_116_269

Perfect score: 154

Sequence: 1 aaggttgccgagagacaa.....ttgttacttccatgttaa 154

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_29Jan04.*

1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002s.*

7: Geneseqn2003as.*

8: Geneseqn2003bs.*

9: Geneseqn2003cs.*

10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	154	100.0	270	2	Aat94582 Amplified
2	154	100.0	286	2	Aat94574 Alyssum s
3	154	100.0	481	2	Aat95289 Alyssum s
4	140.2	91.0	500	2	Aat94581 Composite
5	122.6	79.6	394	9	Adc51221 Brassica
6	122.6	79.6	426	9	Adc51223 Brassica
7	119.4	77.5	243	7	Ada68378 Arabidops
8	119.4	77.5	403	2	Aav10632 A. thalia
9	117.8	76.5	243	6	Abq82690 Wasabia j
10	117.8	76.5	243	6	Abz14241 Arabidops
11	117.8	76.5	243	7	Abz42136 Arabidops
12	117.8	76.5	400	2	Aav10633 A. thalia
13	117.8	76.5	414	2	Aaq38650 Rs-AFP1 c
14	117.8	76.5	414	2	Aaq70128 Antimicro
15	117.8	76.5	414	2	Aat72333 Raphanus
16	117.8	76.5	414	2	Aat68696 Radish an
17	117.8	76.5	414	3	Aaz39123 Wasabia j
18	116.2	75.5	243	6	Abq82691 Wasabia j
19	116.2	75.5	416	3	Aaz39124 Wasabia j
20	116.2	75.5	1616	2	Aav10646 A. thalia
21	115.4	74.9	308	2	Aat94577 Cloned 5'
22	113	73.4	261	2	Aaq38652 Rs-AFP2 c
23	113	73.4	288	2	Aaq70130 Antimicro

24	113	73.4	522	3	AAZ99324	Aaz99324 DNA encod
25	113	73.4	534	3	AAZ51396	Aaz51396 Portion o
26	113	73.4	534	3	AAZ99327	Aaz99327 DNA encod
27	113	73.4	534	3	AAZ99325	Aaz99325 DNA encod
28	113	73.4	606	3	AAZ99326	Aaz99326 DNA encod
29	110.6	71.8	306	2	AAT94580	Aat94580 Cloned 3'
30	109.8	71.3	449	3	AAZ51390	AAZ51390 Raphanus
31	106.6	69.2	485	3	AAZ99337	Aaz99337 DNA encod
32	105	68.2	434	3	AAZ99332	Aaz99332 DNA encod
33	105	68.2	437	3	AAZ99331	Aaz99331 DNA encod
34	105	68.2	443	3	AAZ99330	Aaz99330 DNA encod
35	105	68.2	446	3	AAZ99329	Aaz99329 DNA encod
36	105	68.2	485	3	AAZ99333	Aaz99333 DNA encod
37	105	68.2	485	3	AAZ99335	Aaz99335 DNA encod
38	105	68.2	488	3	AAZ99338	Aaz99338 DNA encod
39	105	68.2	557	3	AAZ99336	Aaz99336 DNA encod
40	105	68.2	575	3	AAZ99339	Aaz99339 DNA encod
41	103.6	67.3	1093	3	AAZ99334	Aaz99334 DNA encod
42	98.6	64.0	1973	3	AAQ46924	Aac46924 Arabidops
43	75.8	49.2	284	2	AAQ38651	Aaq38651 Truncated
44	75.8	49.2	284	2	AAQ70129	Aaq70129 Antimicro
45	45.2	29.4	577	3	AAZ51378	Aaz51378 Dahlia me

ALIGNMENTS

RESULT 1
AAT94582
ID AAT94582 standard; DNA; 270 BP.
XX
AC AAT94582;
XX
DT 12-MAY-1998 (first entry)
XX
DE DE
XX
KW Amplified Alyssum species antifungal polypeptide gene from pMON22652.
KW Antifungal polypeptide; AlyAPP; inhibition; transgenic plant;
KW phytopathogenic fungus; resistance; ss.
XX Alyssum sp.
XX
FH Key Location/Qualifiers
CDS 22..261
FT /*tag= a
FT /product= "AlyAPP antifungal polypeptide"
FT sig_peptide 22..108
FT /*tag= b
FT mat_peptide 109..258
FT /*tag= c
XX
XX WO9737024-A2.
XX
XX 09-OCT-1997.
XX
XX 27-MAR-1997; 97WO-US005709.
XX
XX 29-MAR-1996; 96US-00627706.
XX
XX (MONS) MONSANTO CO.
XX
XX Liang J, Shah D, Wu Y, Rosenberger CA;
XX
XX WPI; 1997-503109/46.
XX P-PSDB; AAW35560.
XX
XX Alyssum antifungal polypeptide and corresponding DNA - used in the
XX production of transgenic plants resistant to phytopathogenic fungi.
XX
XX Example 4; Page 69; 92pp; English.
XX
XX This sequence represents the cDNA sequence cloned into the E. coli
XX cassette vector pMON22317 to generate vector pMON22652. The cDNA encodes

CC the antifungal polypeptide AlyAPP, isolated from plants of the genus
 CC Alyssum. The AlyAPP polypeptide can be used to control phytopathogenic
 CC fungi, whilst the coding DNA can be used to produce transgenic plants
 CC that express the polypeptide making them resistant to the phytopathogenic
 CC fungi.

XX Sequence 270 BP; 75 A; 58 C; 60 G; 75 T; 0 U; 2 Other;

Query Match 100.0%; Score 154; DB 2; Length 270;
 Best Local Similarity 100.0%; Pred. No. 1.9e-42;
 Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATG 60
 |||||
 DB 108 AAGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATG 167
 |||||

QY 61 CAGGAACCAATGCAGAAACCTTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCC 120
 |||||
 DB 168 CAGGAACCAATGCAGAAACCTTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCC 227
 |||||

QY 121 AGCTCACAAATGTATTGTATTCTTCCCATGTTAA 154
 |||||
 DB 228 AGCTCACAAATGTATTGTATTCTTCCCATGTTAA 261
 |||||

RESULT 2
 AAT94574
 ID AAT94574 standard; cDNA; 286 BP.

XX AC AAT94574;
 XX DT 12-MAY-1998 (first entry)
 XX DE Alyssum species anti-fungal polypeptide AlyAPP cDNA sequence.

XX KW Antifungal polypeptide; AlyAPP; inhibition; transgenic plant;
 XX KW phytopathogenic fungus; resistance; ss.

XX OS Alyssum sp.

XX FH Key Location/Qualifiers
 XX CDS 117..269
 FT /*tag= a
 FT /*product= "mature AlyAPP protein"
 FT /*note= "no start codon given at 5' end of sequence"

XX WO9737024-A2.

XX PN 09-OCT-1997.

XX PD 27-MAR-1997; 97WO-US005709.

XX PF 29-MAR-1996; 96US-00627706.

XX PR (MONS) MONSANTO CO.

XX PA Liang J, Shah D, Wu Y, Rosenberger CA;
 XX PI WPI; 1997-503109/46.
 XX DR P-PSDB; AAW35558.

XX PT Alyssum antifungal polypeptide and corresponding DNA - used in the
 XX PT production of transgenic plants resistant to phytopathogenic fungi.

XX PS Claim 12; Page 68; 92pp; English.

XX CC This sequence encodes the mature protein of an antifungal polypeptide
 CC (AlyAPP) isolated from plants of the genus Alyssum. The sequence was PCR
 CC amplified using primers AAT94583-T94584, and the resultant 264 bp
 CC fragment was cloned as a BamHI fragment into the expression vector
 CC pMON2317 to generate plasmid pMON22652. The AlyAPP sequence in this
 CC plasmid is placed under control of an E35S promoter and the maize HSP70
 CC intron I sequence. The protein can be used to control phytopathogenic

CC fungi, whilst the DNA can be used to produce transgenic plants that
 CC express the protein making them resistant to the phytopathogenic fungi

XX Sequence 286 BP; 80 A; 62 C; 65 G; 79 T; 0 U; 0 Other;

Query Match 100.0%; Score 154; DB 2; Length 286;
 Best Local Similarity 100.0%; Pred. No. 2e-42;
 Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATG 60
 |||||
 DB 116 AAGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATG 175
 |||||

QY 61 CAGGAACCAATGCAGAAACCTTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCC 120
 |||||
 DB 176 CAGGAACCAATGCAGAAACCTTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCC 235
 |||||

QY 121 AGCTCACAAATGTATTGTATTCTTCCCATGTTAA 154
 |||||
 DB 236 AGCTCACAAATGTATTGTATTCTTCCCATGTTAA 269
 |||||

RESULT 3
 AAT9289
 ID AAT9289 standard; DNA; 481 BP.

XX AC AAT9289;
 XX DT 12-MAY-1998 (first entry)
 XX DE Alyssum species AlyAPP cDNA sequence.

XX KW Antifungal polypeptide; AlyAPP; inhibition; transgenic plant;
 XX KW phytopathogenic fungus; resistance; ss.

XX OS Alyssum sp.

XX FH Key Location/Qualifiers
 XX CDS 53..292
 FT /*tag= a
 FT /*product= "AlyAPP antifungal polypeptide"
 FT sig_peptide 53..139
 FT /*tag= b
 FT mat_peptide 140..289
 FT /*tag= c
 FT polyA_signal 439..443
 FT /*tag= d

XX WO9737024-A2.

XX PN 09-OCT-1997.

XX PD 27-MAR-1997; 97WO-US005709.

XX PR 29-MAR-1996; 96US-00627706.

XX PA (MONS) MONSANTO CO.

XX PI Liang J, Shah D, Wu Y, Rosenberger CA;
 XX DR WPI; 1997-503109/46.
 XX DR P-PSDB; AAW35560.

XX PT Alyssum antifungal polypeptide and corresponding DNA - used in the
 XX PT production of transgenic plants resistant to phytopathogenic fungi.

XX PS Example 4; Fig 1; 92pp; English.

XX CC This sequence represents the cDNA sequence which encodes the antifungal
 CC polypeptide AlyAPP, isolated from plants of the genus Alyssum. The AlyAPP
 CC polypeptide can be used to control phytopathogenic fungi, whilst the
 CC coding DNA can be used to produce transgenic plants that express the
 CC polypeptide making them resistant to the phytopathogenic fungi

XX SQ Sequence 481 BP; 147 A; 88 C; 91 G; 154 T; 0 U; 1 Other;

Query Match 100.0%; Score 154; DB 2; Length 481;
Best Local Similarity 100.0%; Pred. No. 2.4e-42;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGTTCTGCGAGAGACCAAGTGGGACATGCTCAGGAGTTGTGCGAACAACATGCATG 60
DB 139 AAGTTGTGCGAGAGACCAAGTGGGACATGCTCAGGAGTTGTGCGAACAACATGCATG 198

QY 61 CAGGAACCAATGCGAGAACCTTTGAAAGAGCAGACACGGATCTTGCAACTATGCTTCCC 120
DB 199 CAGGAACCAATGCGAGAACCTTTGAAAGAGCAGACACGGATCTTGCAACTATGCTTCCC 258

QY 121 AGCTCACAAATGTAATTTGTTACTCTCCCATGTAA 154
DB 259 AGCTCACAAATGTAATTTGTTACTCTCCCATGTAA 292

RESULT 4
AAT94581
ID AAT94581 standard; DNA; 500 BP.
XX
AC AAT94581;
XX
DT 12-MAY-1998 (first entry)
XX
DE Composite cDNA sequence for Alyssum species antifungal polypeptide.
XX
KW Antifungal polypeptide; AlyAFP; inhibition; transgenic plant;
KW phytopathogenic fungus; resistance; ss.
XX
OS Alyssum sp.
XX
PN WO9737024-A2.
XX
PD 09-OCT-1997.
XX
PF 27-MAR-1997; 97MO-US005709.
XX
PR 29-MAR-1996; 96US-00627706.
XX
PA (MONS) MONSANTO CO.
XX
PI Liang J, Shah D, Wu Y, Rosenberger CA;
XX
DR WPI; 1997-503109/46.
XX
PT Alyssum antifungal polypeptide and corresponding DNA - used in the
PT production of transgenic plants resistant to phytopathogenic fungi.
XX
PS Example 4; Page 67; 92pp; English.
XX
CC This sequence represents the cDNA sequence encoding the antifungal
CC polypeptide AlyAFP, from plants of the genus Alyssum. The sequence
CC represents a composite of the sequences isolated by 5' and 3' RACE (Rapid
CC Amplification of cDNA Ends) methods (see AAT94577 and AAT94580). The
CC AlyAFP polypeptide can be used to control phytopathogenic fungi, whilst
CC the coding DNA can be used to produce transgenic plants that express the
CC polypeptide making them resistant to the phytopathogenic fungi
XX
SQ Sequence 500 BP; 145 A; 89 C; 111 G; 154 T; 0 U; 1 Other;

Query Match 91.0%; Score 140.2; DB 2; Length 500;
Best Local Similarity 94.8%; Pred. No. 1.3e-37;
Matches 145; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2 AGGTTGTGCGAGAGACCAAGTGGGACATGCTCAGGAGTTGTGCGAACAACATGCATGC 61
DB 159 AAGTTGTGCGAGAGTCCAAAGTGGGAACATGGTTCAGCGGTGTGGGAATAATAACGCATGC 218
QY 62 AGGAACCAATGCGAGAACCTTTGAAAGAGCAGACACGGATCTTGCAACTATGCTTCCCA 121

DB 219 AGGAACCAATGCGAGAACCTTTGAAAGAGCAGACACGGATCTTGCAACTATGCTTCCCA 278

QY 122 GCTCACAAATGTAATTTGTTACTCTCCCATGTAA 154
DB 279 GCTCACAAATGTAATTTGTTACTCTCCCATGTAA 311

RESULT 5
ADC51221
ID ADC51221 standard; DNA; 394 BP.
XX
AC ADC51221;
XX
DT 18-DEC-2003 (first entry)
XX
DE Brassica oleracea defensin protein coding sequence.
XX
KW antimicrobial protein; defensin; transgenic plant;
KW composite disease resistance; pathogenic bacteria;
KW rice white leaf blight; brown-stripe disease; glume blight;
KW seedling damping-off disease; filamentous fungi; rice blight;
KW sheath blight disease; leaf blight; gene; ds.
XX
OS Brassica oleracea.
XX
FH Key Location/Qualifiers
FT CDS 1..243
FT FT /*tag= a
FT FT /product= "Brassica oleracea defensin protein"
XX
PN JP2003088379-A.
XX
PD 25-MAR-2003.
XX
PF 18-SEP-2001; 2001JP-00283117.
XX
PR 18-SEP-2001; 2001JP-00283117.
XX
PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
XX
DR WPI; 2003-621123/59.
DR P-PSDB; ADC51222.
XX
PT Novel protein from Brassica campestris, useful as antimicrobial against
PT plant pathogenic filamentous fungi or pathogenic bacteria, especially for
PT treating e.g. rice white leaf blight and sheath blight disease.
XX
PS Claim 3; SEQ ID NO 1; 34pp; Japanese.
XX
CC The invention comprises the amino acid and coding sequences of
CC antimicrobial (defensin) proteins from Brassica. The DNA and protein
CC sequences of the invention are useful for producing transformed plants
CC with composite disease resistance, especially resistant to diseases
CC caused by pathogenic bacteria, such as: rice white leaf blight, brown-
CC stripe disease, glume blight, and seedling damping-off disease. As well
CC as diseases caused by filamentous fungi, such as: rice blight, sheath
CC blight disease, and leaf blight. The present DNA sequence encodes a
CC Brassica defensin protein of the invention.
XX
SQ Sequence 394 BP; 116 A; 71 C; 82 G; 125 T; 0 U; 0 Other;

Query Match 79.6%; Score 122.6; DB 9; Length 394;
Best Local Similarity 87.6%; Pred. No. 1.2e-31;
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 2 AGGTTGTGCGAGAGACCAAGTGGGACATGCTCAGGAGTTGTGCGAACAACATGCATGC 61
DB 91 AAGTTGTGCGAGAGGCCCAAGTGGGACATGCTCAGGAGTTGTGGAACATAACGCATGC 150

QY 62 AGGAACCAATGCGAGAACCTTTGAAAGAGCAGACACGGATCTTGCAACTATGCTTCCCA 121
DB 151 AAGAATCAGTGCAATTAACCTTGAGAAAGCAGACATGATCTTGCAACTATGCTTCCCA 210

QY 122 GCTCACAAGTATTTTGTACTTCCCATGTAA 154
 Db 211 GCTCACAAGTATTTTGTACTTCCCATGTAA 243

RESULT 6
 ADC51223
 ID ADC51223 standard; DNA; 426 BP.

XX AC ADC51223;
 XX DT 18-DEC-2003 (first entry)
 XX DE Brassica defensin protein coding sequence.

XX antinicrobial protein; defensin; transgenic plant;
 KW composite disease resistance; pathogenic bacteria;
 KW rice white leaf blight; brown-stripe disease; glume blight;
 KW seedling damping-off disease; filamentous fungi; rice blight;
 KW sheath blight disease; leaf blight; gene; ds.

OS Brassica sp.
 FH Key Location/Qualifiers
 FT CDS 1..243
 FT /*tag= a
 FT /product= "Brassica defensin protein"

XX JF2003088379-A.

XX 25-MAR-2003.

XX 18-SEP-2001; 2001JP-00283117.

XX 18-SEP-2001; 2001JP-00283117.

XX (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.

XX WPI; 2003-621123/59.

XX P-PSDB; ADC51224.

XX Novel protein from Brassica campestris, useful as antimicrobial against
 PT plant pathogenic filamentous fungi or pathogenic bacteria, especially for
 PT treating e.g. rice white leaf blight and sheath blight disease.

XX Claim 3; SEQ ID NO 3; 34pp; Japanese.

XX The invention comprises the amino acid and coding sequences of
 CC antimicrobial (defensin) proteins from Brassica. The DNA and protein
 CC sequences of the invention are useful for producing transformed plants
 CC with composite disease resistance, especially resistant to diseases
 CC caused by pathogenic bacteria, such as: rice white leaf blight, brown-
 CC stripe disease, glume blight, and seedling damping-off disease. As well
 CC as diseases caused by filamentous fungi, such as: rice blight, sheath
 CC blight disease, and leaf blight. The present DNA sequence encodes a
 CC Brassica defensin protein of the invention.

XX Sequence 426 BP; 142 A; 72 C; 84 G; 128 T; 0 U; 0 Other;

Query Match 79.6%; Score 122.6; DB 9; Length 426;
 Best Local Similarity 87.6%; Pred. No. 1.3e-31;
 Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 2 AGTTGTGCGAGACCAAGTGGGACATGTCAGGATTTGTGGACACATGATGC 61
 Db 91 AGTTGTGCGAGAGCCAAAGTGGGACATGTCAGGATCTGTGGAACAATAACGATGC 150

QY 62 AGGAACCAATGCAGAAACCTTTGAAAGACGACAGAACACCGATCTTGCACACTATGTCCTCCCA 121
 Db 151 AAGATCAGTGCATTAACCTTTGAGAAAGCAGCATGGATCTTGCACACTATGTCCTCCCA 210

QY 122 GCTCACAAGTATTTTGTACTTCCCATGTAA 154

Db 211 GCTCACAAGTATTTTGTACTTCCCATGTAA 243

RESULT 7

ADA68378

ID ADA68378 standard; DNA; 243 BP.

XX AC ADA68378;

XX DT 20-NOV-2003 (first entry)

XX Arabidopsis thaliana gene, SEQ ID 747.

XX Plant; bacterial infection; fungal infection; viral infection; ds.

XX Arabidopsis thaliana.

XX WO2003000898-A1.

XX 03-JAN-2003.

XX 22-JUN-2001; 2001WO-IB001105.

XX 22-JUN-2001; 2001WO-IB001105.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
 XX Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;

XX WPI; 2003-175290/17.

XX Identifying at least one gene involved in plant resistance or response to
 PT pathogenic infection for conferring resistance or tolerance to a plant to
 PT bacterial, fungal or viral infection by determining or detecting plant
 PT gene expression.

XX Claim 6; SEQ ID NO 747; 899pp; English.

XX The present invention relates to a method (M1) for identifying genes
 CC involved in plant resistance or response to pathogenic infection. M1
 CC comprises identifying a gene whose expression is significantly altered in
 CC the incompatible interaction of plant gene expression relative to
 CC expression of the gene in an uninfected plant, in a mutant plant that
 CC does not express a gene associated with response to pathogenic infection,
 CC or in a corresponding incompatible or compatible interaction. (M1) is
 CC useful for conferring resistance to resistance or tolerance to a plant to
 CC bacterial, fungal or viral infection. The present sequence was used to
 CC illustrate the invention.

XX Sequence 243 BP; 58 A; 56 G; 59 G; 70 T; 0 U; 0 Other;

Query Match 77.5%; Score 119.4; DB 7; Length 243;
 Best Local Similarity 86.3%; Pred. No. 1.3e-30;
 Matches 132; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 2 AGTTGTGCGAGACCAAGTGGGACATGTCAGGATTTGTGGACACATGATGC 61
 Db 91 AGTTGTGCGAGAGGCCAAAGTGGGACATGTCAGGATTTGTGGACACATGATGC 150

QY 62 AGGAACCAATGCAGAAACCTTTGAAAGACGACAGAACACCGATCTTGCACACTATGTCCTCCCA 121
 Db 151 AAGATCAGTGCATTAACCTTTGAGAAAGCAGCATGGATCTTGCACACTATGTCCTCCCA 210

QY 122 GCTCACAAGTATTTTGTACTTCCCATGTAA 154

Db 211 GCTCACAAGTATTTTGTACTTCCCATGTAA 243

RESULT 8

AAV10632

ID AAV10632 standard; DNA; 403 BP.

```
XX AAV10632;
AC
XX 23-JUN-1998 (first entry)
DT
XX
XX A. thaliana PDF1.1 DNA.
DE
XX
XX Defensin; PDF1.1; protection; plant; pathogen; jasmonate; ethylene;
KW fungi; ss.
XX
XX Arabidopsis thaliana.
OS
XX
XX Key Location/Qualifiers
FH CDS 26..268
FT /*tag= a
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FT mat_peptide 114..265
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FT /*product= "PDF1.1"
FT /*note= "plant defensin"
XX
XX WO9800023-A2.
PN
XX
XX 08-JAN-1998.
PD
XX
XX 20-JUN-1997; 97WO-GB001672.
PF
XX
XX 01-JUL-1996; 96GB-00013753.
PR
XX
XX (ZENE ) ZENECA LTD.
PA
XX
XX Broekaert WF, Thomma BPHJ, Penminckx IAMA, Terras FRG, Manners JM;
PI Kazan K;
XX
XX WPI; 1998-086663/08.
DR
XX P-FSDB; AAW40345.
XX
XX Protecting plants against pathogens by inducing defensin genes - by
XX stimulating ethylene or jasmonate pathways, also new promoter of defensin
XX gene from Arabidopsis.
XX
XX Disclosure; Fig 1; 72pp; English.
XX
XX This sequence encodes the Arabidopsis PDF1.1 gene which is used in a
XX novel method for the protection of plants against pathogens which
XX involves inducing expression of a plant defensin gene by stimulating the
XX jasmonate and/or ethylene pathways. The method is used to induce
XX protection against necrotrophic pathogens, specifically fungi and does
XX not require cytotoxic or potentially harmful chemicals
XX
XX Sequence 403 BP; 112 A; 77 C; 85 G; 129 T; 0 U; 0 Other;
SQ
XX
XX Query Match 77.5%; Score 119.4; DB 2; Length 403;
XX Best Local Similarity 86.3%; Pred. No. 1.5e-30;
XX Matches 132; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
XX
XX 2 AGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGGGAAACAACAATGCATGC 61
XX |
XX 116 AAGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGGGAAACAACAATGCATGC 175
XX |
XX
XX 62 AGGACCAATGCAGAAACCTTGAAGAGACGAGAACACGATCTTGCAACTATGCTTCCCA 121
XX |
XX 176 AAGATCATGTCATTAAACCTTGAAGAGACGAGAACACGATCTTGCAACTATGCTTCCCA 235
XX |
XX 122 GCTCACAATGTATTGTTTACTTCCCATGTTAA 154
XX |
XX 236 GCTCACAATGTATTGTTTACTTCCCATGTTAA 268
XX
XX
XX RESULT 9
XX ABQ82690
XX ID ABQ82690 standard; cDNA; 243 BP.
XX
XX AAV10632;
AC
XX 23-JUN-1998 (first entry)
DT
XX
XX A. thaliana PDF1.1 DNA.
DE
XX
XX Defensin; PDF1.1; protection; plant; pathogen; jasmonate; ethylene;
KW fungi; ss.
XX
XX Arabidopsis thaliana.
OS
XX
XX Key Location/Qualifiers
FH CDS 26..268
FT /*tag= a
FT sig_peptide 26..113
FT /*tag= b
FT mat_peptide 114..265
FT /*tag= c
FT /*product= "PDF1.1"
FT /*note= "plant defensin"
XX
XX WO9800023-A2.
PN
XX
XX 08-JAN-1998.
PD
XX
XX 20-JUN-1997; 97WO-GB001672.
PF
XX
XX 01-JUL-1996; 96GB-00013753.
PR
XX
XX (ZENE ) ZENECA LTD.
PA
XX
XX Broekaert WF, Thomma BPHJ, Penminckx IAMA, Terras FRG, Manners JM;
PI Kazan K;
XX
XX WPI; 1998-086663/08.
DR
XX P-FSDB; AAW40345.
XX
XX Protecting plants against pathogens by inducing defensin genes - by
XX stimulating ethylene or jasmonate pathways, also new promoter of defensin
XX gene from Arabidopsis.
XX
XX Disclosure; Fig 1; 72pp; English.
XX
XX This sequence encodes the Arabidopsis PDF1.1 gene which is used in a
XX novel method for the protection of plants against pathogens which
XX involves inducing expression of a plant defensin gene by stimulating the
XX jasmonate and/or ethylene pathways. The method is used to induce
XX protection against necrotrophic pathogens, specifically fungi and does
XX not require cytotoxic or potentially harmful chemicals
XX
XX Sequence 403 BP; 112 A; 77 C; 85 G; 129 T; 0 U; 0 Other;
SQ
XX
XX Query Match 77.5%; Score 119.4; DB 2; Length 403;
XX Best Local Similarity 86.3%; Pred. No. 1.5e-30;
XX Matches 132; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
XX
XX 2 AGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGGGAAACAACAATGCATGC 61
XX |
XX 116 AAGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGGGAAACAACAATGCATGC 175
XX |
XX
XX 62 AGGACCAATGCAGAAACCTTGAAGAGACGAGAACACGATCTTGCAACTATGCTTCCCA 121
XX |
XX 176 AAGATCATGTCATTAAACCTTGAAGAGACGAGAACACGATCTTGCAACTATGCTTCCCA 235
XX |
XX 122 GCTCACAATGTATTGTTTACTTCCCATGTTAA 154
XX |
XX 236 GCTCACAATGTATTGTTTACTTCCCATGTTAA 268
XX
XX
XX RESULT 9
XX ABQ82690
XX ID ABQ82690 standard; cDNA; 243 BP.
XX
XX ABQ82690;
AC
XX 02-JAN-2003 (first entry)
DT
XX
XX Wasabia japonica gamma-thionin encoding cDNA SEQ ID NO:1.
DE
XX
XX Wasabia japonica; gamma-thionin; plant; disease-resistant plant; gene;
KW ss.
XX
XX Eutrema wasabi.
OS
XX
XX Key Location/Qualifiers
FH CDS 1..243
FT /*tag= a
FT /*product= "gamma-thionin"
XX
XX JP2002272292-A.
PN
XX
XX 24-SEP-2002.
PD
XX
XX 22-MAR-2001; 2001JP-00083526.
PF
XX
XX 22-MAR-2001; 2001JP-00083526.
PR
XX
XX (IWAT-) IWATE KEN.
PA
XX
XX WPI; 2002-718704/78.
DR
XX P-FSDB; ABP53725.
XX
XX A disease-resistant plant in which wasabi gamma-thionin gene is
XX introduced, creation of the disease-resistant plant.
XX
XX Claim 3; Page 8; 11pp; Japanese.
XX
XX The present invention describes a disease-resistant plant in which a
XX wasabi gamma-thionin gene is introduced. Also described is a method for
XX the creation of the above disease-resistant plant by introducing a wasabi
XX gamma-thionin gene to a plant. The present sequence encodes a Eutrema
XX wasabi (Wasabia japonica) gamma-thionin protein from the present
XX invention
XX
XX Sequence 243 BP; 60 A; 54 C; 55 G; 74 T; 0 U; 0 Other;
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XX
XX Query Match 76.5%; Score 117.8; DB 6; Length 243;
XX Best Local Similarity 85.6%; Pred. No. 4.4e-30;
XX Matches 131; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
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XX 2 AGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGGGAAACAACAATGCATGC 61
XX |
XX 91 AAGTTGTGCGAGAGTCAAGTGGGACATGGTCAGGAGTCTGTGGAACAACAATCGGTGC 150
XX |
XX
XX 62 AGGACCAATGCAGAAACCTTGAAGAGACGAGAACACGATCTTGCAACTATGCTTCCCA 121
XX |
XX 151 AAGATCATGTCATTAAACCTTGAAGAGACGAGAACACGATCTTGCAACTATGCTTCCCA 210
XX |
XX 122 GCTCACAATGTATTGTTTACTTCCCATGTTAA 154
XX |
XX 211 TATCAGATGTATCTGTTACTTCCCATGTTAA 243
XX
XX
XX RESULT 10
XX ABZ14241
XX ID ABZ14241 standard; DNA; 243 BP.
XX
XX AC ABZ14241;
XX
XX 21-JAN-2003 (first entry)
DT
XX
XX Arabidopsis thaliana stress regulated gene SEQ ID NO 2046.
DE
XX Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX
```

OS Arabidopsis thaliana.
 PN WO200216655-A2.
 PD 28-FEB-2002.
 XX
 XX 24-AUG-2001; 2001WO-US026685.
 XX
 XX 24-AUG-2000; 2000US-0227866P.
 PR 26-JAN-2001; 2001US-0264647P.
 PR 22-JUN-2001; 2001US-0300111P.
 XX
 XX (SCRI) SCRIPPS RES INST.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 XX Harper JF, Kreps J, Wang X, Zhu T;
 PI WPI; 2002-304127/34.
 DR
 XX
 XX Identifying a stress condition to which a plant cell has been exposed and
 PT producing plants with increased tolerance to these abiotic stresses.
 XX
 XX Claim 144; SEQ ID NO 246; 577pp + Sequence Listing; English.
 PS
 XX The invention relates to identifying a stress condition to which a plant
 CC cell has been exposed, comprising: (a) contacting nucleic acid
 CC representative of expressed polynucleotides in the plant cell with an
 CC array or probes representative of the plant cell genome; and (b)
 CC detecting a profile of expressed polynucleotides in the plant cell
 CC characteristic of a stress response. The method is useful in the
 CC production of transgenic plants, cells and seeds and in producing plants
 CC with increased tolerance to abiotic stress. The present sequence is that
 CC of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used
 CC in methods of the invention. Note: The sequence data for this patent is
 CC not represented in the printed specification but is based on sequence
 CC information supplied to Derwent by the European Patent Office
 XX
 XX Sequence 243 BP; 62 A; 57 C; 58 G; 66 T; 0 U; 0 Other;

Query Match 76.5%; Score 117.8; DB 6; Length 243;
 Best Local Similarity 85.8%; Pred. No. 4.4e-30;
 Matches 131; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
 QY 2 AGTTGTGCGAGAGACCAAGTGGACATGTCAGGAGTTTGTGGGAACAACAATGATGC 61
 Db 91 AAGTTGTGCGAGAGACCAAGTGGACATGTCAGGAGTTTGTGGGAACAACAATGATGC 150
 QY 62 AGAACAATGCGAGAAACCTTGAAGAGAGACAGGATCTTGGCAACTATGCTTCCCA 121
 Db 151 AAGAATCAGTGCATTAACTTGAAGAGAGCAACATGGATCATGCAACTATGCTTCCCA 210
 QY 122 GCTCACAATGATTTGTACTTCCCATGTTAA 154
 Db 211 GCACAAGTATCTGTTACGTCCTCATGTTAA 243

RESULT 11
 AB242136
 ID AB242136 standard; cDNA; 243 BP.
 XX
 AC AB242136;
 XX
 DT 27-FEB-2003 (first entry)
 XX
 XX Arabidopsis thaliana gene #120 modulated by PTGS.
 DE
 XX Posttranscriptional gene silencing; PTGS; plant; transformation; gene;
 KW ss.
 XX
 XX Arabidopsis thaliana.
 OS
 XX Key Location/Qualifiers
 FH 1. .243
 FT CDS

FT
 XX
 PN WO200281695-A2.
 XX
 PD 17-OCT-2002.
 XX
 XX 05-APR-2002; 2002WO-EP003806.
 XX
 XX 06-APR-2001; 2001US-0282049P.
 PR
 XX (SYGN) SYNGENTA PARTICIPATIONS AG.
 PA (FRIE-) FRIEDRICH MIESCHER INST.
 XX
 XX Zhu T, Glazov EA, Meins F, Wang X, Chang H;
 PI WPI; 2003-103337/09.
 DR P-PSDB; ABP81292.
 DR
 XX
 XX Novel polynucleic acid segment useful for modulating gene expression
 PT within a cell by posttranscriptional gene silencing, and for augmenting a
 PT plant cell genome.
 XX
 XX Claim 18; Page 425-426; 438pp; English.
 PS
 XX The invention relates to a novel isolated polynucleic acid segment
 CC modulated within a cell by posttranscriptional gene silencing (PTGS). The
 CC invention specifically relates to a method to identify an expression
 CC product that is modulated by PTGS. The polynucleotide is useful for
 CC modulating the gene expression within a cell by PTGS, by introducing the
 CC polynucleic acid into a cell and expressing the nucleic acid segment in
 CC the cell to form a product. The polynucleic acid segment is also useful
 CC for augmenting a cell genome, and for augmenting a plant genome, by
 CC contacting a plant cell with the segment to produce a transformed plant
 CC cell, and growing the transformed plant cell to produce a differentiated
 CC transformed plant. The sequences shown in AB242017 - AB242142 represent
 CC segments of A. thaliana cDNA modulated by PTGS
 XX
 XX Sequence 243 BP; 62 A; 57 C; 58 G; 66 T; 0 U; 0 Other;

Query Match 76.5%; Score 117.8; DB 7; Length 243;
 Best Local Similarity 85.6%; Pred. No. 4.4e-30;
 Matches 131; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
 QY 2 AGTTGTGCGAGAGACCAAGTGGACATGTCAGGAGTTTGTGGGAACAACAATGATGC 61
 Db 91 AAGTTGTGCGAGAGACCAAGTGGACATGTCAGGAGTTTGTGGGAACAACAATGATGC 150
 QY 62 AGAACAATGCGAGAAACCTTGAAGAGAGACAGGATCTTGGCAACTATGCTTCCCA 121
 Db 151 AAGAATCAGTGCATTAACTTGAAGAGAGCAACATGGATCATGCAACTATGCTTCCCA 210
 QY 122 GCTCACAATGATTTGTACTTCCCATGTTAA 154
 Db 211 GCACAAGTATCTGTTACGTCCTCATGTTAA 243

RESULT 12
 AAV10633
 ID AAV10633 standard; DNA; 400 BP.
 XX
 AC AAV10633;
 XX
 DT 23-JUN-1998 (first entry)
 XX
 XX A. thaliana PDF1.2 DNA.
 DE
 XX Defensin; PDF1.2; protection; plant; pathogen; jasmonate; ethylene;
 KW fungi; ss.
 XX
 XX Arabidopsis thaliana.
 OS
 XX Key Location/Qualifiers
 FH 32. .274
 FT CDS

FT sig_peptide /*tag= a
 FT 32..119 /*tag= b
 FT mat_peptide 120..271 /*tag= c
 FT /product= "PDF1.2"
 FT /note= "plant defensin"
 XX

XX W09800023-A2.

XX 08-JAN-1998.

XX 20-JUN-1997; 97WO-GB001672.

XX 01-JUL-1996; 96GB-00013753.

XX (ZENE) ZENECA LTD.

XX Broekaert WF, Thomma BPHJ, Penninckx IAMA, Terras FRG, Manners JM;
 XX Kazan K;

XX WPI; 1998-086663/08.

XX P-PSDB; AAW40346.

XX Protecting plants against pathogens by inducing defensin genes - by
 XX stimulating ethylene or jasmonate pathways, also new promoter of defensin
 XX gene from Arabidopsis.

XX Disclosure; Fig 1; 72pp; English.

XX This sequence encodes the Arabidopsis PDF1.2 gene which is used in a
 XX novel method for the protection of plants against pathogens which
 XX involves inducing expression of a plant defensin gene by stimulating the
 XX jasmonate and/or ethylene pathways. The method is used to induce
 XX protection against necrotrophic pathogens, specifically fungi and does
 XX not require cytotoxic or potentially harmful chemicals

XX Sequence 400 BP; 109 A; 82 C; 80 G; 125 T; 0 U; 4 Other;

Query Match 76.5%; Score 117.8; DB 2; Length 400;
 Best Local Similarity 85.6%; Pred. No. 5.4e-30;
 Matches 131; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
 QY 2 AGGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGGGAAACAACATGCATGC 61
 DB 122 AAGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGGGAAACAAGTAATGCATGC 181

QY 62 AGGAACCAATGCAGAAACCTTGAAGAGACGAGAACACGGATCTTGCATATGCTTCCCA 121

DB 182 AAGAATCAGTGCATTAACCTTGAAGAGAGCCAAACATGGATCATGCAACTATGCTTCCCA 241

QY 122 GCTCACAATGTATTTGTTACTTCCCATGTTAA 154

DB 242 GCACACAAGTGTATCTGTTACGTCCTCCATGTTAA 274

RESULT 13

AAQ38650
 ID AAQ38650 standard; DNA; 414 BP.

XX AAQ38650;

XX 25-MAR-2003 (revised)

XX 07-JUL-1993 (first entry)

XX Rs-APF1 cDNA.

XX Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria;
 KW fungicide; bactericide; antibiotic; antifungal; gram positive;
 KW plant disease resistance; low toxicity.

XX Raphanus sativus.

XX

PH Key Location/Qualifiers
 FT CDS 16..256
 FT /*tag= a

XX W09305153-A1.

XX 18-MAR-1993.

XX 27-AUG-1992; 92WO-GB001570.

XX 29-AUG-1991; 91GB-00018523.

XX 13-FEB-1992; 92GB-00003038.

XX 25-JUN-1992; 92GB-00013526.

XX (ICIL) IMPERIAL CHEM IND PLC.

XX Broekaert WF, Cammue BPA, Osborn RW, Rees SB, Terras FRG;

XX Vanderleyden J;

XX WPI; 1993-100978/12.

XX Biotidal proteins isolated from seeds of plants - e.g. brassica or
 XX dahlia, useful for increasing plants' resistance to fungal and bacterial
 XX diseases.

XX Example 21; Fig 35; 110pp; English.

XX This cDNA represents the sequence of Rs-APF1 from Raphanus sativus. PCR
 XX primer AAQ38640 was used together with AAQ38641 to generate a probe for
 XX screening a Raphanus sativus seed cDNA library. This primer corresponds
 XX to amino acids 2 to 7 of Rs-APF1 and has a sense orientation. The 144bp
 XX product was partially re-amplified using AAQ38642 and AAQ38641 to give a
 XX 123bp product, which was further reamplified with the same primers and
 XX digoxigenin-11-dUTP instead of dTTP to give a digoxigenin labeled PCR
 XX product. This was used to screen a lambda ZAPII cDNA library by in situ
 XX plaque hybridisation. Positive plaques were purified and subjected to two
 XX additional screening rounds with the same probe. Inserts were excised in
 XX vivo into the pBluescript phagemid form with the aid of helper phage
 XX R408. Inserts from 22 positive clones were excised by EcoRI digestion and
 XX their size compared by agarose gel electrophoresis. Four clones had
 XX insert sizes of approx. 400bp the others between 250-300bp. The inserts
 XX of the 4 largest clones were then sequenced and found to differ only in
 XX the length of their 5' and 3' UTR's. The longest sequence is given here.
 XX (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;

Query Match 76.5%; Score 117.8; DB 2; Length 414;
 Best Local Similarity 85.6%; Pred. No. 5.5e-30;
 Matches 131; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 2 AGGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGGGAAACAACATGCATGC 61

DB 106 AAGTTGTGCGAAAGGCCAAGTGGGACATGTCAGGAGTCTGTGGAACAATACCGCATGC 165

QY 62 AGGAACCAATGCAGAAACCTTGAAGAGACGAGAACACGGATCTTGCATATGCTTCCCA 121

DB 166 AAGAATCAGTGCATTAACCTTGAAGAAACGACGACATGATCTTGCATATGCTTCCCA 225

QY 122 GCTCACAATGTATTTGTTACTTCCCATGTTAA 154

DB 226 GCTCACAAGTGTATCTGCTACTTCTTCTTGTAA 258

RESULT 14

AAQ70128
 ID AAQ70128 standard; cDNA; 414 BP.

XX AAQ70128;

XX 25-MAR-2003 (revised)

XX 14-FEB-1995 (first entry)

XX

```

DE Antimicrobial Rs-APPI.
XX
XX Antimicrobial; Rs-APPI; symbiosis; disease-resistance; fungus-resistance;
KW Clavibacter xyli subsp. cynodontis; Cxc; crop improvement; endophyte; ss.
XX
XX Raphanus sativus.
XX
XX WO9416076-A1.
XX
XX 21-JUL-1994.
XX
XX 05-JAN-1994; 94WO-GB000012.
XX
XX 08-JAN-1993; 93GB-00000281.
XX
XX (ZENE ) ZENECA LTD.
XX
XX Dubock AC, Powell KA, Rees SB;
XX WPI; 1994-249223/30.
XX P-PSDB; AAR57325.
XX
XX Antimicrobial protein producing endo-symbiotic microorganisms - is
PT produced by combining nucleic acids encoding the protein with an
PT endophyte, useful for protecting plant hosts from esp. fungal disease.
XX
XX Disclosure; Page 31; 39pp; English.
XX
XX Plant-derived antimicrobial proteins are expressed in endosymbiotic
CC Clavibacter xyli subsp. cynodontis (Cxc). Plants or seeds treated with
CC recombinant Cxc are protected against fungal disease. A suitable
CC antimicrobial protein is Rs-APPI from R. sativus. The full-length cDNA
CC sequence of Rs-APPI is given in AAQ70128. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
XX Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
XX
Query Match 76.5%; Score 117.8; DB 2; Length 414;
Best Local Similarity 85.6%; Pred. No. 5.5e-30;
Matches 131; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 2 AGTTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAACAACATGATGC 61
DB 106 AAGTTGTGCGAAGGCGCAAGTGGGACATGTCAGGAGTCTGTGGAAACAATAACGCATGC 165
QY 62 AGGAACCAATGCAAAACCTTGAAGAGCAGACACGATCTTGCAACTATGCTTCCCA 121
DB 166 AAGATCAGTGCATTAACTTGAAGAAGCAGACATGATGCTTGCAACTATGCTTCCCA 225
QY 122 GCTCACAATGTTATTTGTTACTTCCCATGTAA 154
DB 226 GCTCACAAGTGATCTGCTACTTTCCTTGTAA 258
RESULT 15
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XX AAT72333 standard; cDNA; 414 BP.
XX
XX AAT72333;
XX
XX 25-MAR-2003 (revised)
DT 19-JAN-1998 (first entry)
XX
XX Raphanus sativus antifungal protein I (Rs-APPI) cDNA.
XX
XX Antifungal protein; candida; fungal resistance; food additive; radish;
KW crop protection; plant defensin; bacterial protection; preservative; ss.
XX
XX Raphanus sativus.
XX
XX Key Location/Qualifiers
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FT /*tag= c
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XX
XX WO9721815-A2.
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XX 19-JUN-1997.
XX
XX 12-DEC-1996; 96WO-GB003068.
XX
XX 13-DEC-1995; 95GB-00025455.
XX 28-MAR-1996; 96GB-00006552.
XX
XX (ZENE ) ZENECA LTD.
XX
XX Meloen RH, Puijk WC, Schaaper WM, Sijtsma L, Van Amerongen A;
XX Broekaert W, Samblanx GW, Fant F, Borremans FAM, Rees SB;
XX Van Gelder WMJ;
XX
XX WPI; 1997-332786/30.
XX P-PSDB; AAW19280.
XX
XX Antifungal peptide derived from radish antifungal protein 2 - and related
XX DNA, useful for producing plants with increased fungal resistance and as
XX therapeutic or preservative agent.
XX
XX Claim 8; Fig 2; 65pp; English.
XX
XX This cDNA sequence encodes an Rhanus sativus (radish) antifungal
XX protein (Rs-APPI). Analogues of the homologous protein, Rs-AP2
XX (AAW19281), have also been produced (see AAW19282-92, AAW19294-98,
XX AAW19301-04, AAW19330-34 and AAW1765-834). Plants containing DNA
XX sequences encoding these proteins have improved resistance to fungi.
XX Compositions containing the peptides can be used to control fungi or
XX bacteria in pharmaceutical (e.g. treatment of Candida infections) or
XX preservative purposes (as food additives). In agriculture, the peptide
XX may be used to improve disease resistance or disease tolerance of crops,
XX either pre or post harvest. When applied to plants they may also have
XX curative as well as protective actions. The peptides may also be used to
XX protect plants by introducing them, or a microorganism capable of
XX expressing the peptide into the soil. (Updated on 25-MAR-2003 to correct
XX PI field.)
XX
XX Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
XX
Query Match 76.5%; Score 117.8; DB 2; Length 414;
Best Local Similarity 85.6%; Pred. No. 5.5e-30;
Matches 131; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 2 AGTTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAACAACATGATGC 61
DB 106 AAGTTGTGCGAAGGCGCAAGTGGGACATGTCAGGAGTCTGTGGAAACAATAACGCATGC 165
QY 62 AGGAACCAATGCAAAACCTTGAAGAGCAGACACGATCTTGCAACTATGCTTCCCA 121
DB 166 AAGATCAGTGCATTAACTTGAAGAAGCAGACATGATGCTTGCAACTATGCTTCCCA 225
QY 122 GCTCACAATGTTATTTGTTACTTCCCATGTAA 154
DB 226 GCTCACAAGTGATCTGCTACTTTCCTTGTAA 258
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Job time : 151.15 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 18, 2004, 17:08:11 ; Search time 31.5 Seconds
(without alignments)
2713.093 Million cell updates/sec

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	154	100.0	270	3	US-09-103-489-14
3	154	100.0	270	4	US-09-829-381D-14
4	154	100.0	286	1	US-08-627-706-12
5	154	100.0	286	3	US-09-103-489-12
6	154	100.0	286	4	US-09-829-381D-12
7	140.2	91.0	500	1	US-08-627-706-9
8	140.2	91.0	500	3	US-09-103-489-9
9	140.2	91.0	500	4	US-09-829-381D-9
10	117.8	76.5	414	1	US-08-377-687-48
11	117.8	76.5	414	3	US-08-377-687-48
12	117.8	76.5	414	4	US-08-971-982-48
13	117.8	76.5	414	1	US-08-377-687-48
14	117.8	76.5	414	3	US-08-377-687-48
15	115.4	74.9	308	1	US-08-627-706-5
16	115.4	74.9	308	3	US-09-103-489-5
17	115.4	74.9	308	4	US-09-829-381D-5
18	113	73.4	288	1	US-08-377-687-58
19	113	73.4	288	3	US-08-377-687-58
20	113	73.4	288	4	US-08-971-982-58
21	110.6	71.8	306	1	US-08-627-706-8
22	110.6	71.8	306	3	US-09-103-489-8
23	110.6	71.8	306	4	US-09-829-381D-8
24	109.2	70.9	285	1	US-08-627-706-16
25	109.2	70.9	285	3	US-09-103-489-16
26	109.2	70.9	285	4	US-09-829-381D-16
27	102.8	66.8	285	1	US-08-627-706-17

28	102.8	66.8	285	3	US-09-103-489-17	Sequence 17, Appl
29	102.8	66.8	285	4	US-09-829-381D-17	Sequence 17, Appl
30	75.8	49.2	284	1	US-08-377-687-50	Sequence 50, Appl
31	75.8	49.2	284	1	US-08-777-192-50	Sequence 50, Appl
32	75.8	49.2	284	3	US-08-971-982-50	Sequence 50, Appl
33	42.4	27.5	565	4	US-09-589-733C-6	Sequence 6, Appl
34	39.8	25.8	150	1	US-08-377-687-31	Sequence 31, Appl
35	39.8	25.8	150	1	US-08-377-687-33	Sequence 33, Appl
36	39.8	25.8	150	1	US-08-377-687-34	Sequence 34, Appl
37	39.8	25.8	150	1	US-08-777-192-31	Sequence 31, Appl
38	39.8	25.8	150	1	US-08-777-192-33	Sequence 33, Appl
39	39.8	25.8	150	1	US-08-777-192-34	Sequence 34, Appl
40	39.8	25.8	150	3	US-08-971-982-31	Sequence 31, Appl
41	39.8	25.8	150	3	US-08-971-982-33	Sequence 33, Appl
42	39.8	25.8	150	3	US-08-971-982-34	Sequence 34, Appl
43	35.8	23.2	147	1	US-08-377-687-36	Sequence 36, Appl
44	35.8	23.2	147	1	US-08-777-192-36	Sequence 36, Appl
45	35.8	23.2	147	3	US-08-971-982-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1
US-08-627-706-14
; Sequence 14, Application US/08627706
; Patent No. 5773696
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dillip M.
; APPLICANT: Wu, Yennie S.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, B84F
; STREET: 700 Chesterfield Village Parkway No. 5773696th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/627,706
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21(10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6224
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 270 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-627-706-14

Query Match 100.0%; Score 154; DB 1; Length 270;
Best Local Similarity 100.0%; Pred. No. 2.8e-42;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGTTTGGCAGACCAAGTGGCATGTCAGGAGTTGTGGACACATGATG 60

Db 108 AAGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAACAACAATGCATG 167
QY 61 CAGGAACCAATGCAGAAACCTTGAAGAGCAGAACACGATCTTGCAACTATGTCTTTCCC 120
Db 168 CAGGAACCAATGCAGAAACCTTGAAGAGCAGAACACGATCTTGCAACTATGTCTTTCCC 227
QY 121 AGCTCAAAATGATTTGTTGTTACTTCCCATGTTAA 154
Db 228 AGCTCAAAATGATTTGTTGTTACTTCCCATGTTAA 261

RESULT 2

US-09-103-489-14
; Sequence 14, Application US/09103489
; Patent No. 6215048
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yinnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. 6215048th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/103,489
; FILING DATE: 24-JUN-1998
; CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21 (10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 537-6224
; TELEFAX: (314) 537-6047
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 270 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-103-489-14

Query Match 100.0%; Score 154; DB 3; Length 270;
Best Local Similarity 100.0%; Pred. No. 2.8e-42;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAACAACAATGCATG 60
Db 108 AAGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAACAACAATGCATG 167
QY 61 CAGGAACCAATGCAGAAACCTTGAAGAGCAGAACACGATCTTGCAACTATGTCTTTCCC 120
Db 168 CAGGAACCAATGCAGAAACCTTGAAGAGCAGAACACGATCTTGCAACTATGTCTTTCCC 227
QY 121 AGCTCAAAATGATTTGTTGTTACTTCCCATGTTAA 154
Db 228 AGCTCAAAATGATTTGTTGTTACTTCCCATGTTAA 261

RESULT 3

US-09-829-381D-14
; Sequence 14, Application US/09829381D
; Patent No. 6653280
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yinnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for Control
; TITLE OF INVENTION: Plant Pathogenic Fungi
; FILE REFERENCE: 38-21 (10700) C
; CURRENT APPLICATION NUMBER: US/09/829,381D
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/103,489
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 270
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid
US-09-829-381D-14

Query Match 100.0%; Score 154; DB 4; Length 270;
Best Local Similarity 100.0%; Pred. No. 2.8e-42;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAACAACAATGCATG 60
Db 108 AAGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAACAACAATGCATG 167
QY 61 CAGGAACCAATGCAGAAACCTTGAAGAGCAGAACACGATCTTGCAACTATGTCTTTCCC 120
Db 168 CAGGAACCAATGCAGAAACCTTGAAGAGCAGAACACGATCTTGCAACTATGTCTTTCCC 227
QY 121 AGCTCAAAATGATTTGTTGTTACTTCCCATGTTAA 154
Db 228 AGCTCAAAATGATTTGTTGTTACTTCCCATGTTAA 261

RESULT 4

US-08-627-706-12
; Sequence 12, Application US/08627706
; Patent No. 5773696
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yinnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. 5773696th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/627,706
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565

REFERENCE/DOCKET NUMBER: 38-21(10700)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6224
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-627-706-12

Query Match 100.0%; Score 154; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.9e-42;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAACAACAATGCATG 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 116 AAGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAACAACAATGCATG 175
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 61 CAGGAACCAATGCAGAACCTTGAAGAGCAGACACCGATCTTGCAACTATGCTTCCC 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 176 CAGGAACCAATGCAGAACCTTGAAGAGCAGACACCGATCTTGCAACTATGCTTCCC 235
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 121 AGCTCACAATGTATTGTTACTTCCCATGTTAA 154
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 236 AGCTCACAATGTATTGTTACTTCCCATGTTAA 269
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 5
US-09-103-489-12
Sequence 12, Application US/09103489
Patent No. 6215048
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 6215048th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,489
FILING DATE: 24-JUN-1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-6224
TELEFAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-103-489-12

Query Match 100.0%; Score 154; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.9e-42;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAACAACAATGCATG 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 116 AAGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAACAACAATGCATG 175
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 61 CAGGAACCAATGCAGAACCTTGAAGAGCAGACACCGATCTTGCAACTATGCTTCCC 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 176 CAGGAACCAATGCAGAACCTTGAAGAGCAGACACCGATCTTGCAACTATGCTTCCC 235
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 121 AGCTCACAATGTATTGTTACTTCCCATGTTAA 154
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 236 AGCTCACAATGTATTGTTACTTCCCATGTTAA 269
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 6
US-09-829-381D-12
Sequence 12, Application US/09829381D
Patent No. 6653280
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alyesum and Methods for Control
TITLE OF INVENTION: Plant Pathogenic Fungi
FILE REFERENCE: 38-21 (10700) C
CURRENT APPLICATION NUMBER: US/09/829,381D
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/103,489
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 286
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic PCR reaction product
US-09-829-381D-12

Query Match 100.0%; Score 154; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.9e-42;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAACAACAATGCATG 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 116 AAGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAACAACAATGCATG 175
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 61 CAGGAACCAATGCAGAACCTTGAAGAGCAGACACCGATCTTGCAACTATGCTTCCC 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 176 CAGGAACCAATGCAGAACCTTGAAGAGCAGACACCGATCTTGCAACTATGCTTCCC 235
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 121 AGCTCACAATGTATTGTTACTTCCCATGTTAA 154
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 236 AGCTCACAATGTATTGTTACTTCCCATGTTAA 269
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 7
US-08-627-706-9
Sequence 9, Application US/08627706
Patent No. 5773696
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 19

```
/
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
/ STREET: 700 Chesterfield Village Parkway No. 5773696th
/ CITY: St. Louis
/ STATE: Missouri
/ COUNTRY: USA
/ ZIP: 63198
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/627,706
/ FILING DATE:
/ CLASSIFICATION: 436
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Cohen, Charles E.
/ REGISTRATION NUMBER: 34,565
/ REFERENCE/DOCKET NUMBER: 38-21 (10700) A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (314) 537-6224
/ TELEFAX: (314) 537-6047
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 500 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ US-08-627-706-9

Query Match          91.0%; Score 140.2; DB 1; Length 500;
Best Local Similarity 94.8%; Pred. No. 1.4e-37;
Matches 145; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2 AGGTTGTGGGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACATGCGATGC 61
Db 159 AAGTTGTGGGAGAGTCCAAAGTGGAAATGGTCAGGCGTGTGGGAATAATAACGCGATGC 218
QY 62 AGGAACCAATGCAGAAACCTTGAAGAGCAGACACGGATCTTGCACATGCTTTCCCA 121
Db 219 AGGAACCAATGCAGAAACCTTGAAGAGCAGACACGGATCTTGCACATGCTTTCCCA 278
QY 122 GCTCAAAATGTTTGTACTTCCCATGTTAA 154
Db 279 GCTCAAAATGTTTGTACTTCCCATGTTAA 311

RESULT 8
US-09-103-489-9
; Sequence 9, Application US/09103489
; Patent No. 6215048
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yennie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. 6215048th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
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/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/103,489
/ FILING DATE: 24-JUN-1998
/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Cohen, Charles E.
/ REGISTRATION NUMBER: 34,565
/ REFERENCE/DOCKET NUMBER: 38-21 (10700) A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (314) 537-6224
/ TELEFAX: (314) 537-6047
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 500 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ US-09-103-489-9

Query Match          91.0%; Score 140.2; DB 3; Length 500;
Best Local Similarity 94.8%; Pred. No. 1.4e-37;
Matches 145; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2 AGGTTGTGGGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACATGCGATGC 61
Db 159 AAGTTGTGGGAGAGTCCAAAGTGGAAATGGTCAGGCGTGTGGGAATAATAACGCGATGC 218
QY 62 AGGAACCAATGCAGAAACCTTGAAGAGCAGACACGGATCTTGCACATGCTTTCCCA 121
Db 219 AGGAACCAATGCAGAAACCTTGAAGAGCAGACACGGATCTTGCACATGCTTTCCCA 278
QY 122 GCTCAAAATGTTTGTACTTCCCATGTTAA 154
Db 279 GCTCAAAATGTTTGTACTTCCCATGTTAA 311

RESULT 9
US-09-829-381D-9
; Sequence 9, Application US/09829381D
; Patent No. 6653280
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yennie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide ALYAAP from Alyssum and Methods for Control
; TITLE OF INVENTION: Plant Pathogenic Fungi
; FILE REFERENCE: 38-21 (10700) C
; CURRENT APPLICATION NUMBER: US/09/829,381D
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/103,489
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 500
; TYPE: DNA
; ORGANISM: Alyssum spp
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (22)..(22)
; OTHER INFORMATION: N = any nucleotide
/ US-09-829-381D-9

Query Match          91.0%; Score 140.2; DB 4; Length 500;
Best Local Similarity 94.8%; Pred. No. 1.4e-37;
Matches 145; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2 AGGTTGTGGGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACATGCGATGC 61
Db 159 AAGTTGTGGGAGAGTCCAAAGTGGAAATGGTCAGGCGTGTGGGAATAATAACGCGATGC 218
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Qy 62 AGGAACCAATCGAGAAACCTTTGAAGAGCAGACACGCGATCTTGCAACTATGTCTTCCCA 121
Db 219 AGGAACCAATCGAGAAACCTTTGAAGAGCAGACACGCGATCTTGCAACTATGTCTTCCCA 278
Qy 122 GCTCACAATGTTATTTGTTACTTCCCATGTTAA 154
Db 279 GCTCACAATGTTATTTGTTACTTCCCATGTTAA 311

RESULT 10

US-08-377-687-48
; Sequence 48, Application US/08377687
; Patent No. 5538525
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEIDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/377,687
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SER.36525/US/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..255
US-08-377-687-48

Query Match 76.5%; Score 117.8; DB 1; Length 414;
Best Local Similarity 85.6%; Pred. No. 4.2e-30;
Matches 131; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
Qy 2 AGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGAGTTCTGGGAACAACAATGCCATGC 61
Db 106 AAGTTGTGCGAAAGCCCAAGTGGGACATGGTCAGAGTCTGGGAACAACAATGCCATGC 165
Qy 62 AGGAACCAATCGAGAAACCTTTGAAGAGCAGACACGCGATCTTGCAACTATGTCTTCCCA 121
Db 166 AAGAATCAGTGCATTAACTTTGAGAAACGACGACATGGATCTTGCAACTATGTCTTCCCA 225
Qy 122 GCTCACAATGTTATTTGTTACTTCCCATGTTAA 154

Db 226 GCTCACAAGTGATCTGCTACTTTCCTTGTTAA 258

RESULT 11

US-08-777-192-48
; Sequence 48, Application US/08777192
; Patent No. 5824869
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEIDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,192
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SER.36525/US/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..255
US-08-777-192-48

Query Match 76.5%; Score 117.8; DB 1; Length 414;
Best Local Similarity 85.6%; Pred. No. 4.2e-30;
Matches 131; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
Qy 2 AGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGAGTTCTGGGAACAACAATGCCATGC 61
Db 106 AAGTTGTGCGAAAGCCCAAGTGGGACATGGTCAGAGTCTGGGAACAACAATGCCATGC 165
Qy 62 AGGAACCAATCGAGAAACCTTTGAAGAGCAGACACGCGATCTTGCAACTATGTCTTCCCA 121
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RESULT 12

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US-08-971-982-48
; Sequence 48, Application US/08971982
; Patent No. 6187904
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; CAMMUE, BRUNO P.A.
; OSBORN, RUPERT W.
; REES, SARAH B.
; TERRAS, FRANKY R.G.
; VANDERLEIDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971.982
; FILING DATE: 17-No. 6187904-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SER.36525/US/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 48:
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..255
; SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-08-971-982-48
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Best Local Similarity 85.6%; Pred. No. 4.2e-30;
Matches 131; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 2 AGTTGTGCGAGACCAAGTGGACATGTTCAGGAGTTTGTGGGAACAACAATGCATGC 61
Db 106 AAGTTGTGCGAAAGGCCAAGTGGACATGTTCAGGAGTTTGTGGGAACAACAATGCATGC 165
QY 62 AGGAACAATGCAGAACCTTGAAGAGCAGACACGATCTTGCACACTATGCTTCCCA 121
Db 166 AGAATCAGTGCAATTAACCTTGAGAAAGCAGCATGGATCTTGCACACTATGCTTCCCA 121
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Db 226 GCTCACAAGTGTATCTGCTACTTCTTGTAA 258
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US-09-077-948A-45
; Sequence 45, Application US/09077948A
; Patent No. 6605698
; GENERAL INFORMATION:
; APPLICANT: Van Amerongen, Aart
; APPLICANT: Fant, Franky
; APPLICANT: Borremans, Frans
; APPLICANT: De Samblanx, Genoveva
; APPLICANT: Sitjtsma, Lolke
; APPLICANT: Meloen, Robbert
; APPLICANT: Puijk, Wouter
; APPLICANT: Schaaper, Wilhelmus
; APPLICANT: Broekaert, Willem
; APPLICANT: Van Gelder, Wilhelmus
; APPLICANT: Rees, Sarah
; TITLE OF INVENTION: Antifungal Proteins
; FILE REFERENCE: 109846-257(SYN-035)
; CURRENT APPLICATION NUMBER: US/09/077,948A
; CURRENT FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: PCT/GB96/03068
; PRIOR FILING DATE: 1996-12-12
; PRIOR APPLICATION NUMBER: GB 9606552.9
; PRIOR FILING DATE: 1996-03-28
; PRIOR APPLICATION NUMBER: GB 9525455.3
; PRIOR FILING DATE: 1995-12-13
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 414
; TYPE: DNA
; ORGANISM: Raphanus sativus
US-09-077-948A-45
Query Match 76.5%; Score 117.8; DB 4; Length 414;
Best Local Similarity 85.6%; Pred. No. 4.2e-30;
Matches 131; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 2 AGTTGTGCGAGACCAAGTGGACATGTTCAGGAGTTTGTGGGAACAACAATGCATGC 61
Db 106 AAGTTGTGCGAAAGGCCAAGTGGACATGTTCAGGAGTTTGTGGGAACAACAATGCATGC 165
QY 62 AGGAACAATGCAGAACCTTGAAGAGCAGACACGATCTTGCACACTATGCTTCCCA 121
Db 166 AGAATCAGTGCAATTAACCTTGAGAAAGCAGCATGGATCTTGCACACTATGCTTCCCA 121
QY 122 GCTCACAAGTGTATTTGTTACTTCCCATGTTAA 154
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US-08-971-982-48
Query Match 76.5%; Score 117.8; DB 3; Length 414;
Best Local Similarity 85.6%; Pred. No. 4.2e-30;
Matches 131; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 2 AGTTGTGCGAGACCAAGTGGACATGTTCAGGAGTTTGTGGGAACAACAATGCATGC 61
Db 106 AAGTTGTGCGAAAGGCCAAGTGGACATGTTCAGGAGTTTGTGGGAACAACAATGCATGC 165
QY 62 AGGAACAATGCAGAACCTTGAAGAGCAGACACGATCTTGCACACTATGCTTCCCA 121
Db 166 AGAATCAGTGCAATTAACCTTGAGAAAGCAGCATGGATCTTGCACACTATGCTTCCCA 121
QY 122 GCTCACAAGTGTATTTGTTACTTCCCATGTTAA 154
Db 226 GCTCACAAGTGTATCTGCTACTTCTTGTAA 258
RESULT 13
US-09-077-951-19
; Sequence 19, Application US/09077951
; Patent No. 6372888
; GENERAL INFORMATION:
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Job time : 32.5 secs

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	Matches 128;	Conservative 0;	Mismatches 22;	Indels 0;	Gaps 0;
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Qy	62	AGGAACCAATCCAGAAACCTTTGAAAGAGCAGAAACACGGATCTTGCACATATGTCTTCCCA	121		
Db	219	AAGAAATCAGTGCATTAACCTTTGAGGAGCAGCAATGGATCTTGCACATATGTCTTCCCA	278		
Qy	122	GCTCACAATGATTTGTTACTTCCCATGT	151		
Db	279	GCTCACAAGTGCATATGCTATCTTCCCCTGT	308		

Query Match 74.9%; Score 115.4; DB 1; Length 308;
Best Local Similarity 85.3%; Pred. No. 2.4e-29;
Matches 128; Conservative 0; Mismatches 22; Indels 0

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 18, 2004, 17:59:12 ; Search time 141.75 Seconds

(without alignments)
4930.226 Million cell updates/sec

Title: US-10-681-972-12_COPY_116_269

Perfect score: 154

Sequence: 1 aaggtgtgcagagaccaa.....tttgttacttcccatgtaa 154

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2947324 seqs, 2269024515 residues

Total number of hits satisfying chosen parameters: 5894648

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
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- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
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- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
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- 17: /cgn2_6/ptodata/1/pubpna/US10E_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	154	100.0	270	13	US-10-681-972-14
3	154	100.0	286	9	US-09-829-381A-12
4	154	100.0	286	13	US-10-681-972-12
5	140.2	91.0	500	9	US-09-829-381A-9
6	140.2	91.0	500	13	US-10-681-972-9
7	119.4	77.5	403	9	US-09-732-561-13
8	117.8	76.5	243	11	US-09-938-842A-2046
9	117.8	76.5	243	11	US-09-938-842A-2046
10	117.8	76.5	400	9	US-09-732-561-15
11	117.8	76.5	400	9	US-09-887-576-607
12	117.8	76.5	414	9	US-09-759-584-48
13	117.8	76.5	414	13	US-10-388-361A-45
14	117.8	76.5	414	14	US-10-006-252A-19

15	116.2	75.5	1616	9	US-09-732-561-21
16	115.4	74.9	308	9	US-09-829-381A-5
17	115.4	74.9	308	13	US-10-681-972-5
18	113	73.4	288	9	US-09-759-584-58
19	110.6	71.8	306	9	US-09-829-381A-8
20	110.6	71.8	306	13	US-10-681-972-8
21	109.2	70.9	285	9	US-09-829-381A-16
22	109.2	70.9	285	13	US-10-681-972-16
23	102.8	66.8	285	9	US-09-829-381A-17
24	102.8	66.8	285	13	US-10-681-972-17
25	75.8	49.2	284	9	US-09-759-584-50
26	54.8	35.6	373	9	US-09-770-696-283
27	43.6	28.3	156	15	US-10-178-449A-34
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29	43.6	28.3	658	15	US-10-178-449A-7
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31	42.6	27.7	457	15	US-10-178-449A-13
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33	42.6	27.7	460	15	US-10-178-449A-17
34	42.6	27.7	463	15	US-10-178-449A-9
35	42.6	27.7	464	15	US-10-178-449A-19
36	42.6	27.7	472	15	US-10-178-449A-23
37	42.6	27.7	603	15	US-10-178-449A-11
38	42.6	27.5	461	15	US-10-178-449A-46
39	42.4	27.5	565	12	US-10-636-396-6
40	40.2	26.1	501	15	US-10-178-449A-5
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43	39.8	25.8	150	9	US-09-759-584-34
44	39	25.3	529	15	US-10-178-449A-48
45	39	25.3	579	15	US-10-178-449A-31

ALIGNMENTS

RESULT 1

US-09-829-381A-14
; Sequence 14, Application US/09829381A
; Patent No. US20020144306A1

; GENERAL INFORMATION:

; APPLICANT: Liang, Jihong

; Shah, Dilip M.

; Wu, Yonnie S.

; Rosenberger, Cindy A.

; TITLE OF INVENTION: Antifungal Polypeptide and Methods for

; Controlling Plant Pathogenic Fungi

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F

; STREET: 700 Chesterfield Village Parkway No. US20020144306A1th

; CITY: St. Louis

; STATE: Missouri

; COUNTRY: USA

; ZIP: 63198

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/829,381A

; FILING DATE: 09-Apr-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/103,489

; FILING DATE: 1998-06-24

; ATTORNEY/AGENT INFORMATION:

; NAME: Cohen, Charles E.

; REGISTRATION NUMBER: 34,565

; REFERENCE/DOCKET NUMBER: 38-21 (10700)A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (314) 537-6224

Sequence 21, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 58, Appl
Sequence 8, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 283, App
Sequence 34, Appl
Sequence 29, Appl
Sequence 7, Appl
Sequence 15, Appl
Sequence 13, Appl
Sequence 21, Appl
Sequence 17, Appl
Sequence 9, Appl
Sequence 19, Appl
Sequence 23, Appl
Sequence 11, Appl
Sequence 46, Appl
Sequence 6, Appl
Sequence 5, Appl
Sequence 31, Appl
Sequence 33, Appl
Sequence 34, Appl
Sequence 48, Appl
Sequence 31, Appl

TELEFAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 270 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-829-381A-14

Query Match 100.0%; Score 154; DB 9; Length 270;
Best Local Similarity 100.0%; Pred. No. 2.3e-42;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 108 AAGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGATTTGTGGGAACAACAAATGCATG 167
QY 61 CAGGAACCAATGCAGAAACCTTGAAGAGCAGAACACGGATCTTGCACACTATGCTTCCC 120
DB 168 CAGGAACCAATGCAGAAACCTTGAAGAGCAGAACACGGATCTTGCACACTATGCTTCCC 227
QY 121 AGCTCAAAATGATTTGTTACTTCCCATGTTAA 154
DB 228 AGCTCAAAATGATTTGTTACTTCCCATGTTAA 261

RESULT 2

US-10-681-972-14
Sequence 14, Application US/10681972
Publication No. US20040064850A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonnie S.
TITLE OF INVENTION: Antifungal Polypeptide
TITLE OF INVENTION: Plant Pathogenic Fungi
FILE REFERENCE: 38-21 (10700) C
CURRENT APPLICATION NUMBER: US/10/681,972
CURRENT FILING DATE: 2003-10-09
PRIOR APPLICATION NUMBER: US/09/829,381D
PRIOR FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/103,489
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 14
LENGTH: 270
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Plasmid
US-10-681-972-14

Query Match 100.0%; Score 154; DB 13; Length 270;
Best Local Similarity 100.0%; Pred. No. 2.3e-42;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGATTTGTGGGAACAACAAATGCATG 60
DB 108 AAGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGATTTGTGGGAACAACAAATGCATG 167
QY 61 CAGGAACCAATGCAGAAACCTTGAAGAGCAGAACACGGATCTTGCACACTATGCTTCCC 120
DB 168 CAGGAACCAATGCAGAAACCTTGAAGAGCAGAACACGGATCTTGCACACTATGCTTCCC 227
QY 121 AGCTCAAAATGATTTGTTACTTCCCATGTTAA 154
DB 228 AGCTCAAAATGATTTGTTACTTCCCATGTTAA 261

RESULT 3

US-09-829-381A-12
Sequence 12, Application US/09829381A
Patent No. US20020144306A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSER: Charles E. Cohen, Monsanto Company, B84F
STREET: 700 Chesterfield Village Parkway No. US20020144306A1th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/829,381A
FILING DATE: 09-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/103,489
FILING DATE: 1998-06-24
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-6224
TELEFAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-829-381A-12

Query Match 100.0%; Score 154; DB 9; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.4e-42;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 176 CAGGAACCAATGCAGAAACCTTGAAGAGCAGAACACGGATCTTGCACACTATGCTTCCC 235
QY 121 AGCTCAAAATGATTTGTTACTTCCCATGTTAA 154
DB 236 AGCTCAAAATGATTTGTTACTTCCCATGTTAA 269

RESULT 4

US-10-681-972-12
Sequence 12, Application US/10681972
Publication No. US20040064850A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonnie S.

APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alyssum and Methods for Controlling Plant Pathogenic Fungi
FILE REFERENCE: 38-21 (10700) C
CURRENT APPLICATION NUMBER: US/10/681,972
CURRENT FILING DATE: 2003-10-09
PRIOR APPLICATION NUMBER: US/09/829,381D
PRIOR FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/103,489
PRIOR FILING DATE: 1998-06-24
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 286
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic PCR reaction product
US-10-681-972-12

Query Match 100.0%; Score 154; DB 13; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.4e-42;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAACAACATGCGATG 60
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QY 61 CAGGAACCAATGCAGAAACCTTGAAGAGCAGACACGGATCTTGCACACTATGCTTCCC 120
DB 176 CAGGAACCAATGCAGAAACCTTGAAGAGCAGACACGGATCTTGCACACTATGCTTCCC 235
QY 121 AGCTCACAATGTATTTGTTACTTCCCATGTTAA 154
DB 236 AGCTCACAATGTATTTGTTACTTCCCATGTTAA 269

RESULT 5

US-09-829-381A-9
Sequence 9, Application US/09829381A
Patent No. US20020144306A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yonnie S.
Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSER: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. US20020144306A1th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/829,381A
FILING DATE: 09-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/103,489
FILING DATE: 1998-06-24
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700)A
TELECOMMUNICATION INFORMATION:

TELEPHONE: (314) 537-6224
TELEFAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 500 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-829-381A-9

Query Match 91.0%; Score 140.2; DB 9; Length 500;
Best Local Similarity 94.8%; Pred. No. 1.6e-37;
Matches 145; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 2 AGTTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAACAACATGCGATG 61
DB 159 AAGTTTGTGCGAGAGTCCAAGTGGAAACATGTCAGGCGTGTGGGAATAATAACGCGATG 218
QY 62 AGGAACCAATGCAGAAACCTTGAAGAGCAGACACGGATCTTGCACACTATGCTTCCCA 121
DB 219 AGGAACCAATGCAGAAACCTTGAAGAGCAGACACGGATCTTGCACACTATGCTTCCCA 278
QY 122 GCTCACAATGTATTTGTTACTTCCCATGTTAA 154
DB 279 GCTCACAATGTATTTGTTACTTCCCATGTTAA 311

RESULT 6

US-10-681-972-9
Sequence 9, Application US/10681972
Publication No. US20040064850A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
Shah, Dilip M.
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alyssum and Methods for Controlling Plant Pathogenic Fungi
FILE REFERENCE: 38-21 (10700) C
CURRENT APPLICATION NUMBER: US/10/681,972
CURRENT FILING DATE: 2003-10-09
PRIOR APPLICATION NUMBER: US/09/829,381D
PRIOR FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/103,489
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 500
TYPE: DNA
ORGANISM: Alyssum spp
FEATURE:
NAME/KEY: misc feature
LOCATION: (22)-(22)
OTHER INFORMATION: N = any nucleotide
US-10-681-972-9

Query Match 91.0%; Score 140.2; DB 13; Length 500;
Best Local Similarity 94.8%; Pred. No. 1.6e-37;
Matches 145; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 2 AGTTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAACAACATGCGATG 61
DB 159 AAGTTTGTGCGAGAGTCCAAGTGGAAACATGTCAGGCGTGTGGGAATAATAACGCGATG 218
QY 62 AGGAACCAATGCAGAAACCTTGAAGAGCAGACACGGATCTTGCACACTATGCTTCCCA 121
DB 219 AGGAACCAATGCAGAAACCTTGAAGAGCAGACACGGATCTTGCACACTATGCTTCCCA 278
QY 122 GCTCACAATGTATTTGTTACTTCCCATGTTAA 154

Db 279 GCTCAAAATGATTGTTGTTACTTCCCATGTTAA 311

RESULT 7

US-09-732-561-13

; Sequence 13, Application US/09732561

; Patent No. US20020035738A1

; GENERAL INFORMATION:

; APPLICANT: Thoma, Bart

; APPLICANT: Terias, Franky

; APPLICANT: Penninckx, Iris

; APPLICANT: Manners, John

; APPLICANT: Kazan, Kemal

; APPLICANT: Broekaert, Willem

; TITLE OF INVENTION: Plant Protection Method

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:

; ADDRESSER: ZENECA Ag Products

; STREET: 1800 Concord Pike

; CITY: Wilmington

; STATE: DE

; COUNTRY: USA

; ZIP: 19850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/732,561

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/202,638

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB97/01672

; FILING DATE: 20-JUN-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Hohenschutz, Liza D.

; REGISTRATION NUMBER: 33,712

; REFERENCE/DOCKET NUMBER: PPD 50165/UST

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (302) 886-1699

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 403 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; ORIGINAL SOURCE:

; STRAIN: PDF 1.1

US-09-732-561-13

Query Match

Best Local Similarity 77.5%; Score 119.4; DB 9; Length 403;

Matches 132; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 2 AGTTGTGCGAGACCAAGTGGGACATGTCAGGAGTTTGGGAAACAAATGTCATGC 61

Db 116 AAGTTGTGCGAGAGCGCAAGTGGGACATGTCGCGAGTTTGGGAAACAGTAACGCGTGC 175

QY 62 AGGAACCAATGAGAACTTGAAGAGAGACACGAGTTCGCAACTATCTCTTCCCA 121

Db 176 AGAATCATGTGATTACCTTGAGAAAGCAGCATGGAATCTTGAACATGTCCTTCCCA 235

QY 122 GCTCAAAATGATTGTTGTTACTTCCCATGTTAA 154

Db 236 GCTCAAAATGATTGTTGTTACTTCCCATGTTAA 268

RESULT 8

Query Match

Best Local Similarity 76.5%; Score 117.8; DB 11; Length 243;

Matches 131; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

US-09-938-842A-2046

; Sequence 2046, Application US/09938842A

; Patent No. US20020160378A1

; GENERAL INFORMATION:

; APPLICANT: Harper, Jeff

; APPLICANT: Kreps, Joel

; APPLICANT: Wang, Xun

; APPLICANT: Zhu, Tong

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

; FILE REFERENCE: SCRIPI300-3

; CURRENT APPLICATION NUMBER: US/09/938,842A

; CURRENT FILING DATE: 2001-08-24

; PRIOR APPLICATION NUMBER: US 60/227,866

; PRIOR FILING DATE: 2000-08-24

; PRIOR APPLICATION NUMBER: US 60/264,647

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/300,111

; PRIOR FILING DATE: 2001-06-22

; NUMBER OF SEQ ID NOS: 5379

; SEQ ID NO 2046

; LENGTH: 243

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

US-09-938-842A-2046

Query Match

Best Local Similarity 76.5%; Score 117.8; DB 9; Length 243;

Matches 131; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 2 AGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGGGAAACAAATGTCATGC 61

Db 91 AAGTTGTGCGAGACCCAAAGTGGGACATGTCAGGAGTTTGGGAAACAGTAATGTCATGC 150

QY 62 AGGAACCAATGAGAAACCTTGAAGAGAGACAGACGAGTTCGCAACTATCTTCCCA 121

Db 151 AGAATCATGTGCAATTAACCTTGAAGAGAGCAACATGATCATGCAACTATCTTCCCA 210

QY 122 GCTCAAAATGATTGTTGTTACTTCCCATGTTAA 154

Db 211 GCACAAAGTGTATCTGTACGTCCCATGTTAA 243

RESULT 9

US-09-938-842A-2046

; Sequence 2046, Application US/09938842A

; Publication No. US20040009476A9

; GENERAL INFORMATION:

; APPLICANT: Harper, Jeff

; APPLICANT: Kreps, Joel

; APPLICANT: Wang, Xun

; APPLICANT: Zhu, Tong

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

; FILE REFERENCE: SCRIPI300-3

; CURRENT APPLICATION NUMBER: US/09/938,842A

; CURRENT FILING DATE: 2001-08-24

; PRIOR APPLICATION NUMBER: US 60/227,866

; PRIOR FILING DATE: 2000-08-24

; PRIOR APPLICATION NUMBER: US 60/264,647

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/300,111

; PRIOR FILING DATE: 2001-06-22

; NUMBER OF SEQ ID NOS: 5379

; SEQ ID NO 2046

; LENGTH: 243

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

US-09-938-842A-2046

Query Match

Best Local Similarity 76.5%; Score 117.8; DB 11; Length 243;

Matches 131; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Qy	2	AGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGACACCAATGCATGC	61
Db	91	ANGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGACACCAATGCATGC	150
Qy	62	AGGAACCAATCAGAGAAACCTTGAAGAGAGAGAACACGGATCTTGGCAATATGCTTCCCA	121
Db	151	AAGAAATCAGTGCATTAACCTTTGAAGAGAGCCAAACATGGATCATGCAACTATGCTCTCCCA	210
Qy	122	GCTCACAAATGATTTGTTACTTCCCATGTTAA	154
Db	211	GCAACAAGTGATCTGTTACGTCCCATGTTAA	243

```

RESULT 10
US-09-732-561-15
; Sequence 15, Application US/09732561
; Patent No. US20020035738A1
; GENERAL INFORMATION:
; APPLICANT: Thomma, Bart
; APPLICANT: Terras, Franky
; APPLICANT: Penninckx, Iris
; APPLICANT: Manners, John
; APPLICANT: Kazan, Kemal
; APPLICANT: Broekaert, Willem
; TITLE OF INVENTION: Plant Protection Method
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZENECA Ag Products
; STREET: 1800 Concord Pike
; CITY: Wilmington
; STATE: DE
; COUNTRY: USA
; ZIP: 19850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.251
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/732,561
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/202,638
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB97/01672
; FILING DATE: 20-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: PPD 50165/UST
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 886-1699
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 400 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; STRAIN: PFD1.2
US-09-732-561-15

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Query Match	76.5%	Score 117.8	DB 9	Length 400
Best Local Similarity	85.6%	Pred. No. 6.5e-30		
Matches 131	Conservative 0	Mismatches 22	Indels 0	Gaps 0
QY	2	AGGTTGTCGAGAGACCAAGTGGGACATGTTGAGGAGTTTGTGGGAAACAACATGCATGC	61	
Db	122	AAGTTGTCGAGAAAGCCAAAGTGGGACATGTTGAGGAGTTTGTGGGAAACAAGTAATGCATGC	181	

Qy	62	AGAACCAATGCAGAAACCTTGAAGAGCAGAAACGGATCTTGTCAATATCTCTTCCCA	121
Db	182	AAGAAATCAGTGCATTAACCTTGAAGAGGCCAAACATGGATCATGCAACTATCTCTTCCCA	241
Qy	122	GCTCACAATGTATTGTGTTACTTCCCATGTTAA	154
Db	242	GCACACAAGTATCTGTTAGTCCCATGTTAA	274

```

RESULT 11
US-09-887-576-607
; Sequence 607, Application US/09887576
; Patent No. US20020144047A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, P.
; APPLICANT: Brown, D.
; APPLICANT: Chang, H.
; APPLICANT: Zhu, T.
; APPLICANT: Han, B.
; APPLICANT: Wang, X.
; APPLICANT: Cooper, Bret
; TITLE OF INVENTION: Promoters for regulation of plant expression
; FILE REFERENCE: 1360.001US1
; CURRENT APPLICATION NUMBER: US/09/887,576
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/213,848
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/214,087
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/258,692
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 875
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 607
; LENGTH: 400
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(400)
; OTHER INFORMATION: n = A,T,C or G
US-09-887-576-607

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	Query Match	76.5%	Score 117.8	DB 9	Length 400
	Best Local Similarity	85.6%	Pred. No. 6.5e-30		
	Matches 131	Conservative 0	Mismatches 22	Indels 0	Gaps 0
QY	2	AGGTTGTGCAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAACAACATGCATGC	61		
Db	122	AGGTTGTGCAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAACAACATGCATGC	181		
QY	62	AGGAACCAATGCGAGAAACCTTTGAAGACGAGAACACGGATCTTTGCCAACTATGTTCTCCCA	121		
Db	182	AAGAATCAGTGCATTAACCTTTGAAGGACCAACATGGATCATGCAACTATGTTCTCCCA	241		
QY	122	GCTCACAAATGATTTGTTACTTCCCATGTTAA	154		
Db	242	GCACACAAGTGATCTGTTACGTGCCATGTTAA	274		

RESULT 12
US-09-759-584-48
; Sequence 48, Application US/09759584
; Patent No. US20010014732A1
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, ROBERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS

NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DAREY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/759,584
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/377,687
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 414 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 16..255
US-09-759-584-48

Query Match 76.5%; Score 117.8; DB 9; Length 414;
Best Local Similarity 85.6%; Pred. No. 6.6e-30;
Matches 131; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 2 AGGTTGTGGAGAGACCAAGTGGGACATGCTCAGGAGTTTGTGGGAACAACATGCGATGC 61
Db 106 AAGTTGTGGAAAGGCCAAGTGGGACATGCTCAGGAGTCTGTGGAACAATAACGCGATGC 165
QY 62 AGGAACCAATGCAGAAACCTTGAAGAGCAGACACGGATCTTGCACCTATGCTTTCCCA 121
Db 166 AAGAATCAGTGCAATTAACCTTGAGAAAGCAGACATGGATCTTGCACCTATGCTTTCCCA 225
QY 122 GGTCAAAATGATTTGTTACTTCCCATGTTAA 154
Db 226 GGTCAAAATGATCTGCTACTTCTCTGTTAA 258

RESULT 13
US-10-388-361A-45
Sequence 45, Application US/10388361A
Publication No. US20030226169A1
GENERAL INFORMATION:
APPLICANT: Van Amerongen, Aart
APPLICANT: Fant, Franky
APPLICANT: Borremans, Frans
APPLICANT: De Samblanx, Genoveva
APPLICANT: Sitjtsma, Lolke
APPLICANT: Melen, Robbert
APPLICANT: Fuijk, Wouter
APPLICANT: Schaaper, Wilhelms
APPLICANT: Broekaert, Willem
APPLICANT: Van Gelder, Wilhelms
APPLICANT: Rees, Sarah
TITLE OF INVENTION: Antifungal Proteins

FILE REFERENCE: 5C094PPDDIV
CURRENT APPLICATION NUMBER: US/10/388,361A
CURRENT FILING DATE: 2003-03-13
PRIOR APPLICATION NUMBER: US 09/077,948
PRIOR FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: PCT/GB96/03068
PRIOR FILING DATE: 1996-12-12
PRIOR APPLICATION NUMBER: GB 9606552.9
PRIOR FILING DATE: 1996-03-28
PRIOR APPLICATION NUMBER: GB 9525455.3
PRIOR FILING DATE: 1995-12-13
NUMBER OF SEQ ID NOS: 141
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 45
LENGTH: 414
TYPE: DNA
ORGANISM: Raphanus sativus
US-10-388-361A-45

Query Match 76.5%; Score 117.8; DB 13; Length 414;
Best Local Similarity 85.6%; Pred. No. 6.6e-30;
Matches 131; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 2 AGGTTGTGGAGAGACCAAGTGGGACATGCTCAGGAGTTTGTGGGAACAACATGCGATGC 61
Db 106 AAGTTGTGGAAAGGCCAAGTGGGACATGCTCAGGAGTCTGTGGAACAATAACGCGATGC 165
QY 62 AGGAACCAATGCAGAAACCTTGAAGAGCAGACACGGATCTTGCACCTATGCTTTCCCA 121
Db 166 AAGAATCAGTGCAATTAACCTTGAGAAAGCAGACATGGATCTTGCACCTATGCTTTCCCA 225
QY 122 GGTCAAAATGATTTGTTACTTCCCATGTTAA 154
Db 226 GGTCAAAATGATCTGCTACTTCTCTGTTAA 258

RESULT 14
US-10-006-252A-19
Sequence 13, Application US/10006252A
Publication No. US20020152498A1
GENERAL INFORMATION:
APPLICANT: De Samblanx, Genoveva
APPLICANT: Broekaert, Willem
APPLICANT: Rees, Sarah
TITLE OF INVENTION: Antifungal Proteins
FILE REFERENCE: SYN-034DV
CURRENT APPLICATION NUMBER: US/10/006,252A
CURRENT FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 09/077,951
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: GB 9525474.4
PRIOR FILING DATE: 1995-12-13
PRIOR APPLICATION NUMBER: PCT/GB96/03065
PRIOR FILING DATE: 1996-12-12
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 19
LENGTH: 414
TYPE: DNA
ORGANISM: Raphanus sativus
US-10-006-252A-19

Query Match 76.5%; Score 117.8; DB 14; Length 414;
Best Local Similarity 85.6%; Pred. No. 6.6e-30;
Matches 131; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 2 AGGTTGTGGAGAGACCAAGTGGGACATGCTCAGGAGTTTGTGGGAACAACATGCGATGC 61
Db 106 AAGTTGTGGAAAGGCCAAGTGGGACATGCTCAGGAGTCTGTGGAACAATAACGCGATGC 165
QY 62 AGGAACCAATGCAGAAACCTTGAAGAGCAGACACGGATCTTGCACCTATGCTTTCCCA 121
Db 166 AAGAATCAGTGCAATTAACCTTGAGAAAGCAGACATGGATCTTGCACCTATGCTTTCCCA 225

Db 1535 GCACACAAGTGATCTGTTACGTCCCATGTAA 1567

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Job time : 141.75 secsQY 122 GCTCACAAATGATTTGTTACTTCCCATGTAA 154
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Db 226 GCTCACAAAGTGATCTGTTACTTCCCTGTAA 258
|||||

RESULT 15

US-09-732-561-21
; Sequence 21, Application US/09732561
; Patent No. US20020035738A1
; GENERAL INFORMATION:
; APPLICANT: Thomma, Bart
; APPLICANT: Terras, Franky
; APPLICANT: Penninckx, Iris
; APPLICANT: Manners, John
; APPLICANT: Kazan, Kemal
; APPLICANT: Broekaert, Willem
; TITLE OF INVENTION: Plant Protection Method
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZENECA Ag Products
; STREET: 1800 Concord Pike
; CITY: Wilmington
; STATE: DE
; COUNTRY: USA
; ZIP: 19850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/732,561
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/202,638
; FILING DATE:
; PRIOR APPLICATION DATA: PCT/GB97/01672
; APPLICATION NUMBER: 20-JUN-1997
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liiza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: PPD 50165/UST
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 886-1699
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1616 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; STRAIN: Arabidopsis PDF1.2 gene
; INDIVIDUAL ISOLATE: DNA sequence Figure 14
US-09-732-561-21

Query Match 75.5%; Score 116.2; DB 9; Length 1616;
Best Local Similarity 85.0%; Pred. No. 4.1e-29;
Matches 130; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
QY 2 AGGTGTGGCAGAGACCAAGTGGACATGTCAGGAGTTTGTGGGAACACAAATGCATGC 61
|||||
Db 1415 AGTTGTGGCAGAGACCAAGTGGACATGTCAGGAGTTTGTGGGAACACAAATGCATGC 1474
|||||
QY 62 AGGAACCAATGCGAAGAACCTTGAAGACGACGATCTTGCACACTATGTCTTCCCA 121
|||||
Db 1475 AAGAATCAGTGCATTAACCTCGAAGAGCCAAACATGATGCACACTATGTCTTCCCA 1534
|||||
QY 122 GCTCACAAATGATTTGTTACTTCCCATGTAA 154
|||||

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
3225.394 Million cell updates/sec

Title: US-10-681-972-12_COPY_116_269

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 37577330 segs, 17593059518 residues

Total number of hits satisfying chosen parameters: 75154660

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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3: /cgn2_6/ptodata/2/pna/US07 COMB.seq:*

4: /cgn2_6/ptodata/2/pna/US08 COMB.seq:*

5: /cgn2_6/ptodata/2/pna/US09 COMB.seq:*

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14: /cgn2_6/ptodata/2/pna/US099 COMB.seq:*

15: /cgn2_6/ptodata/2/pna/US0991 COMB.seq:*

16: /cgn2_6/ptodata/2/pna/US0992 COMB.seq:*

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38: /cgn2_6/ptodata/2/pna/US099996 COMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMVARIES

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1	154	100.0	270	53	US-10-681-972-14
2	154	100.0	286	53	US-10-681-972-12
3	140.2	91.0	500	53	US-10-681-972-9
4	122.6	79.6	243	30	US-09-708-427-18199
5	122.6	79.6	243	38	US-09-935-625-5250
6	122.6	79.6	243	38	US-09-935-625-5383
7	122.6	79.6	243	38	US-09-935-625-28557
8	122.6	79.6	243	38	US-09-935-625-28943
9	122.6	79.6	584	21	US-09-505-533-7439
10	122.6	79.6	584	33	US-09-819-091A-7439
11	122.6	79.6	61290	22	US-09-534-858-830
12	122.6	79.6	61290	33	US-09-803-736-830
13	122.6	79.6	87080	22	US-09-534-858-284
14	122.6	79.6	87080	33	US-09-803-736-284
15	119.4	77.5	243	30	US-09-708-427-21472
16	119.4	77.5	243	36	US-09-887-272A-747
17	119.4	77.5	243	38	US-09-935-625-5372
18	119.4	77.5	243	38	US-09-935-625-28904
19	119.4	77.5	243	50	US-10-380-710-170
20	119.4	77.5	243	50	US-10-380-710-365
21	119.4	77.5	403	16	US-09-202-638-13
22	119.4	77.5	403	31	US-09-732-561-13
23	119.4	77.5	418	27	US-09-654-617-117133
24	119.4	77.5	418	29	US-09-684-016-117133
25	119.4	77.5	595	21	US-09-505-533-7438
26	119.4	77.5	595	33	US-09-819-091A-7438
27	119.4	77.5	97208	22	US-09-534-858-136
28	119.4	77.5	97208	33	US-09-803-736-136
29	117.8	76.5	243	38	US-09-938-842A-2046
30	117.8	76.5	243	50	US-10-380-710-93
31	117.8	76.5	243	50	US-10-380-710-266
32	117.8	76.5	243	95	US-60-382-898-1141
33	117.8	76.5	243	95	US-60-382-898-1150
34	117.8	76.5	400	16	US-09-202-638-15
35	117.8	76.5	400	31	US-09-732-561-15
36	117.8	76.5	400	36	US-09-887-576-607
37	117.8	76.5	400	46	US-10-177-253-215
38	117.8	76.5	414	5	US-08-178-430-37
39	117.8	76.5	414	8	US-08-452-078-48
40	117.8	76.5	414	31	US-09-759-584-48
41	117.8	76.5	414	43	US-10-006-252A-19
42	117.8	76.5	414	50	US-10-388-361A-45
43	117.8	76.5	439	74	US-60-184-698-919
44	117.8	76.5	715	27	US-09-654-617-132225
45	117.8	76.5	715	29	US-09-684-016-132225

ALIGNMENTS

RESULT 1	
US-10-681-972-14	
Sequence 14, Application US/10681972	
Best Local Similarity 100.0%; Pred. No. 7.1e-39;	
Matches 154; Conservative 0; Mismatches 0; Gaps 0;	
GENERAL INFORMATION:	
APPLICANT: Liang, Jihong	
APPLICANT: Shah, Dilip M.	
APPLICANT: Wu, Yennie S.	
APPLICANT: Rosenberger, Cindy A.	
TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alyssum and Methods for Control	
FILE REFERENCE: 38-21 (10700) C	
CURRENT APPLICATION NUMBER: US/10/681,972	
PRIOR FILING DATE: 2003-10-09	
PRIOR APPLICATION NUMBER: US/09/829,381D	
PRIOR FILING DATE: 2001-04-09	
PRIOR APPLICATION NUMBER: 09/103,489	
NUMBER OF SEQ ID NOS: 20	
SOFTWARE: Patent in version 3.1	

SEQ ID NO 14	
LENGTH: 270	
TYPE: DNA	
ORGANISM: Artificial Sequence	
FEATURE:	
OTHER INFORMATION: Plasmid	
US-10-681-972-14	
Query Match	100.0%; Score 154; DB 53; Length 270;
Best Local Similarity	100.0%; Pred. No. 7.1e-39;
Matches 154; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 AAGTTGTGCGAGAGACCAAGTGGGACATGTCAGAGTTTGTGGGAAACAACATGTCATG 60
Db	108 AAGTTGTGCGAGAGACCAAGTGGGACATGTCAGAGTTTGTGGGAAACAACATGTCATG 167
QY	61 CAGGAACCAATGCAGAAACCTTGAAGAGACAGAACACGATCTTGCAACTATGCTTCCC 120
Db	168 CAGGAACCAATGCAGAAACCTTGAAGAGACAGAACACGATCTTGCAACTATGCTTCCC 227
QY	121 AGCTCAAAATGATTTGTTACTTCCCATGTTAA 154
Db	228 AGCTCAAAATGATTTGTTACTTCCCATGTTAA 261
RESULT 2	
US-10-681-972-12	
Sequence 12, Application US/10681972	
GENERAL INFORMATION:	
APPLICANT: Liang, Jihong	
APPLICANT: Shah, Dilip M.	
APPLICANT: Wu, Yennie S.	
APPLICANT: Rosenberger, Cindy A.	
TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alyssum and Methods for Control	
FILE REFERENCE: 38-21 (10700) C	
CURRENT APPLICATION NUMBER: US/10/681,972	
CURRENT FILING DATE: 2003-10-09	
PRIOR APPLICATION NUMBER: US/09/829,381D	
PRIOR FILING DATE: 2001-04-09	
PRIOR APPLICATION NUMBER: 09/103,489	
PRIOR FILING DATE: 1998-06-24	
NUMBER OF SEQ ID NOS: 20	
SOFTWARE: Patent in version 3.1	
SEQ ID NO 12	
LENGTH: 286	
TYPE: DNA	
ORGANISM: Artificial Sequence	
FEATURE:	
OTHER INFORMATION: Synthetic PCR reaction product	
US-10-681-972-12	
Query Match	100.0%; Score 154; DB 53; Length 286;
Best Local Similarity	100.0%; Pred. No. 7.3e-39;
Matches 154; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 AAGTTGTGCGAGAGACCAAGTGGGACATGTCAGAGTTTGTGGGAAACAACATGTCATG 60
Db	116 AAGTTGTGCGAGAGACCAAGTGGGACATGTCAGAGTTTGTGGGAAACAACATGTCATG 175
QY	61 CAGGAACCAATGCAGAAACCTTGAAGAGACAGAACACGATCTTGCAACTATGCTTCCC 120
Db	176 CAGGAACCAATGCAGAAACCTTGAAGAGACAGAACACGATCTTGCAACTATGCTTCCC 235
QY	121 AGCTCAAAATGATTTGTTACTTCCCATGTTAA 154
Db	236 AGCTCAAAATGATTTGTTACTTCCCATGTTAA 269
RESULT 3	
US-10-681-972-9	
Sequence 9, Application US/10681972	
GENERAL INFORMATION:	

APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide ALYAFF from Alyesum and Methods for Control
FILE REFERENCE: 38-21 (10700) C
CURRENT APPLICATION NUMBER: US/10/681,972
CURRENT FILING DATE: 2003-10-09
PRIOR APPLICATION NUMBER: US/09/829,381D
PRIOR FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/103,489
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 500
TYPE: DNA
ORGANISM: Alyesum spp
FEATURE:
NAME/KEY: misc feature
LOCATION: (22)-(22)
OTHER INFORMATION: N = any nucleotide
US-10-681-972-9

Query Match 91.0%; Score 140.2; DB 53; Length 500;
Best Local Similarity 94.8%; Pred. No. 2.5e-34;
Matches 145; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2 AGTTGTGCGAGACCAAGTGGGACATGTCAGAGTTTGTGGGAAACAATGCAATGC 61
DB 159 AAGTTGTGCGAGAGTCCAAAGTGGGACATGTCAGGCGTGTGGGAAATAAAGCGCATGC 218

QY 62 AGGAACCAATCGAAGACCTTGAAGAGCAGACACCGATCTTCAACTATGTTCTTCCCA 121
DB 219 AGGAACCAATCGAAGACCTTGAAGAGCAGACACCGATCTTCAACTATGTTCTTCCCA 278

QY 122 GCTCACAATGTAATTTGTTACTTCCCATGTTAA 154
DB 279 GCTCACAATGTAATTTGTTACTTCCCATGTTAA 311

RESULT 4
US-09-708-427-18199
Sequence 18199, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 18199
LENGTH: 243
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..243
OTHER INFORMATION: any n = a, g, c, t, unknown, or other
NAME/KEY: misc feature
LOCATION: 1..243
OTHER INFORMATION: Ceres Seq. ID 1833757
US-09-708-427-18199

Query Match 79.6%; Score 122.6; DB 30; Length 243;
Best Local Similarity 87.6%; Pred. No. 9.8e-29;
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 2 AGTTGTGCGAGACCAAGTGGGACATGTCAGAGTTTGTGGGAAACAATGCAATGC 61

Db 91 AAGTTGTGCGAGACCAAGTGGTACTTGGTCAGAGTTTGGGAAACAATGCAATGC 150
QY 62 AGGAACCAATCGAAGACCTTGAAGAGCAGACACCGATCTTGAACATATGTTCTTCCCA 121
Db 151 AAGAATCAGTGCATTAACCTTGAAGAGGAGCAAAACATGATCTTGCAACTATGTTCTTCCCA 210
QY 122 GCTCACAATGTAATTTGTTACTTCCCATGTTAA 154
Db 211 GCTCACAAGTATCTGTTACGTCCCATGTTAA 243

RESULT 5
US-09-935-625-5250
Sequence 5250, Application US/09935625
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPABLE
FILE REFERENCE: 2750-1481P
CURRENT APPLICATION NUMBER: US/09/935,625
CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 33136
SEQ ID NO 5250
LENGTH: 243
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: Misc feature
LOCATION: 1..243
OTHER INFORMATION: Ceres Seq. ID no. 2143607
US-09-935-625-5250

Query Match 79.6%; Score 122.6; DB 38; Length 243;
Best Local Similarity 87.6%; Pred. No. 9.8e-29;
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 2 AGTTGTGCGAGACCAAGTGGGACATGTCAGAGTTTGTGGGAAACAATGCAATGC 61
Db 91 AAGTTGTGCGAGAGCAAGTGGGACATGTCAGCGCTTTCGGGAAACAGTAATGCAATGC 150

QY 62 AGGAACCAATCGAAGACCTTGAAGAGCAGACACCGATCTTGAACATATGTTCTTCCCA 121
Db 151 AAGAATCAGTGCATTAACCTTGAAGAGGAGCAAAACATGATCTTGCAACTATGTTCTTCCCA 210

QY 122 GCTCACAATGTAATTTGTTACTTCCCATGTTAA 154
Db 211 GCTCACAATGTAATCTGTTACGTCCCATGTTAA 243

RESULT 6
US-09-935-625-5383
Sequence 5383, Application US/09935625
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPABLE
FILE REFERENCE: 2750-1481P
CURRENT APPLICATION NUMBER: US/09/935,625
CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 33136
SEQ ID NO 5383
LENGTH: 243
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: Misc feature
LOCATION: 1..243
OTHER INFORMATION: Ceres Seq. ID no. 2711695
US-09-935-625-5383

Query Match 79.6%; Score 122.6; DB 38; Length 243;
Best Local Similarity 87.6%; Pred. No. 9.8e-29;
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 2 AGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAACAACATGCAATGC 61
Db 91 AAGTTGTGCGAGAGACCAAGTGGTACTTGTGTCAGGAGTTTGTGGGAACAACATGCAATGC 150
QY 62 AGGAACCAATGCGAAGAACCTTTGAAAGAGCAGAACACCGATCTTTGCAACTATGCTTCCCA 121
Db 151 AAGAATCAGTGCATTAACCTTGAAGGAGCAAAACATGGATCTTTGCAACTATGCTTCCCA 210
QY 122 GCTCACAATGATTTGTTACTTCCCATGTAA 154
Db 211 GCTCACAATGATTTGTTACTTCCCATGTAA 243

RESULT 7

US-09-935-625-28557
; Sequence 28557, Application US/09935625
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPABLE
; FILE REFERENCE: 2750-1481P
; CURRENT APPLICATION NUMBER: US/09/935,625
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 33136
; SEQ ID NO 28557
; LENGTH: 243
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; NAME/KEY: Misc_feature
; LOCATION: 1..243
; OTHER INFORMATION: Ceres Seq. ID no. 2143607
US-09-935-625-28557

Query Match 79.6%; Score 122.6; DB 38; Length 243;
Best Local Similarity 87.6%; Pred. No. 9.8e-29;
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 2 AGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAACAACATGCAATGC 61
Db 91 AAGTTGTGCGAGAGACCAAGTGGTACTTGTGTCAGGAGTTTGTGGGAACAACATGCAATGC 150
QY 62 AGGAACCAATGCGAAGAACCTTTGAAAGAGCAGAACACCGATCTTTGCAACTATGCTTCCCA 121
Db 151 AAGAATCAGTGCATTAACCTTGAAGGAGCAAAACATGGATCTTTGCAACTATGCTTCCCA 210
QY 122 GCTCACAATGATTTGTTACTTCCCATGTAA 154
Db 211 GCTCACAATGATTTGTTACTTCCCATGTAA 243

RESULT 8

US-09-935-625-28943
; Sequence 28943, Application US/09935625
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPABLE
; FILE REFERENCE: 2750-1481P
; CURRENT APPLICATION NUMBER: US/09/935,625
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 33136
; SEQ ID NO 28943
; LENGTH: 243
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; NAME/KEY: Misc_feature
; LOCATION: 1..243
; OTHER INFORMATION: Ceres Seq. ID no. 2711695
US-09-935-625-28943

Query Match 79.6%; Score 122.6; DB 38; Length 243;
Best Local Similarity 87.6%; Pred. No. 9.8e-29;
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 2 AGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAACAACATGCAATGC 61
Db 91 AAGTTGTGCGAGAGACCAAGTGGTACTTGTGTCAGGAGTTTGTGGGAACAACATGCAATGC 150
QY 62 AGGAACCAATGCGAAGAACCTTTGAAAGAGCAGAACACCGATCTTTGCAACTATGCTTCCCA 121
Db 151 AAGAATCAGTGCATTAACCTTGAAGGAGCAAAACATGGATCTTTGCAACTATGCTTCCCA 210
QY 122 GCTCACAATGATTTGTTACTTCCCATGTAA 154
Db 211 GCTCACAATGATTTGTTACTTCCCATGTAA 243

RESULT 9

US-09-505-532-7439/c
; Sequence 7439, Application US/09505532
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Plant Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15478)B
; CURRENT APPLICATION NUMBER: US/09/505,532
; CURRENT FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: USSN 60/120,645 1999-02-18; USSN 09/443,025 1999-11-12;
; PRIOR FILING DATE: USSN 60/120,645 1999-02-18; USSN 09/443,025 1999-11-12;
; NUMBER OF SEQ ID NOS: 51470
; SEQ ID NO 7439
; LENGTH: 584
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-505-532-7439

Query Match 79.6%; Score 122.6; DB 21; Length 584;
Best Local Similarity 87.6%; Pred. No. 1.3e-28;
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 2 AGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAACAACATGCAATGC 61
Db 290 AAGTTGTGCGAGAGACCAAGTGGTACTTGTGTCAGGAGTTTGTGGGAACAACATGCAATGC 231
QY 62 AGGAACCAATGCGAAGAACCTTTGAAAGAGCAGAACACCGATCTTTGCAACTATGCTTCCCA 121
Db 230 AAGAATCAGTGCATTAACCTTGAAGGAGCAAAACATGGATCTTTGCAACTATGCTTCCCA 171
QY 122 GCTCACAATGATTTGTTACTTCCCATGTAA 154
Db 170 GCTCACAATGATTTGTTACTTCCCATGTAA 138

RESULT 10

US-09-819-091A-7439/c
; Sequence 7439, Application US/09819091A
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Plant Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15478)B
; CURRENT APPLICATION NUMBER: US/09/819,091A
; CURRENT FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: US 60/108,420
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: US 60/120,645
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 09/443,025
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 51470
; SEQ ID NO 7439
; LENGTH: 584
; TYPE: DNA


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; ORGANISM: Arabidopsis thaliana
US-09-819-091A-7439

Query Match
Best Local Similarity 79.6%; Score 122.6; DB 33; Length 584;
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 2 AGTTGTGCGAGAGACCAAGTGGGACATGGTTCAGGAGTTTGTGGGAAACAACATGCAATGC 61
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 62 AGGAACCAATGCAGAACCTTGAAGAGCAGACACGATCTTGCACATATGCTTCCCA 121
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 230 AAGAATCAGTGCATTAACCTTGAAGAGCAGACACATGGATCTTGCACATATGCTTCCCA 171
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 122 GCTCACAATGTATTTGTTACTTCCCATGTTAA 154
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 11
US-09-534-859-830/c
; Sequence 830, Application US/09534859
; GENERAL INFORMATION:
; APPLICANT: Bush, David F.
; APPLICANT: Last, Robert L.
; APPLICANT: Levin, Irena M.
; APPLICANT: Norris, Susan R.
; APPLICANT: Parnell, Laurence D.
; APPLICANT: Rounsley, Steven D.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: PLANT POLYMORPHIC MARKERS AND USES THEREOF
; FILE REFERENCE: 38-10(15493)B
; CURRENT APPLICATION NUMBER: US/09/534,859
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 1127
; SEQ ID NO 830
; LENGTH: 61290
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-534-859-830

Query Match
Best Local Similarity 79.6%; Score 122.6; DB 22; Length 61290;
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 2 AGTTGTGCGAGAGACCAAGTGGGACATGGTTCAGGAGTTTGTGGGAAACAACATGCAATGC 61
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 62 AGGAACCAATGCAGAACCTTGAAGAGCAGACACGATCTTGCACATATGCTTCCCA 121
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 22629 AAGAATCAGTGCATTAACCTTGAAGAGCAGACACATGGATCTTGCACATATGCTTCCCA 22570
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 122 GCTCACAATGTATTTGTTACTTCCCATGTTAA 154
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 12
US-09-803-736-830/c
; Sequence 830, Application US/09803736
; GENERAL INFORMATION:
; APPLICANT: Bush, David F.
; APPLICANT: Levin, Irena M.
; APPLICANT: Norris, Susan R.
; APPLICANT: Rounsley, Steven D.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof
; FILE REFERENCE: 38-10(15493)D
; CURRENT APPLICATION NUMBER: US/09/803,736
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 09/534,859
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; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: identified by Attorney Docket number 04983.0206CPUS01 38-10.
; NUMBER OF SEQ ID NOS: 1582
; SEQ ID NO 830
; LENGTH: 61290
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-803-736-830

Query Match
Best Local Similarity 79.6%; Score 122.6; DB 33; Length 61290;
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 2 AGTTGTGCGAGAGACCAAGTGGGACATGGTTCAGGAGTTTGTGGGAAACAACATGCAATGC 61
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 62 AGGAACCAATGCAGAACCTTGAAGAGCAGACACGATCTTGCACATATGCTTCCCA 121
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 22629 AAGAATCAGTGCATTAACCTTGAAGAGCAGACACATGGATCTTGCACATATGCTTCCCA 22570
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 122 GCTCACAATGTATTTGTTACTTCCCATGTTAA 154
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 22569 GCTCACAATGTATCTGTTCATGCTCCCATGTTAA 22537
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 13
US-09-534-859-284/c
; Sequence 284, Application US/09534859
; GENERAL INFORMATION:
; APPLICANT: Bush, David F.
; APPLICANT: Last, Robert L.
; APPLICANT: Levin, Irena M.
; APPLICANT: Norris, Susan R.
; APPLICANT: Parnell, Laurence D.
; APPLICANT: Rounsley, Steven D.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: PLANT POLYMORPHIC MARKERS AND USES THEREOF
; FILE REFERENCE: 38-10(15493)B
; CURRENT APPLICATION NUMBER: US/09/534,859
; CURRENT FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 1127
; SEQ ID NO 284
; LENGTH: 87080
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-534-859-284

Query Match
Best Local Similarity 79.6%; Score 122.6; DB 22; Length 87080;
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 2 AGTTGTGCGAGAGACCAAGTGGGACATGGTTCAGGAGTTTGTGGGAAACAACATGCAATGC 61
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 62 AGGAACCAATGCAGAACCTTGAAGAGCAGACACGATCTTGCACATATGCTTCCCA 121
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 54990 AAGAATCAGTGCATTAACCTTGAAGAGCAGACACATGGATCTTGCACATATGCTTCCCA 54931
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 122 GCTCACAATGTATTTGTTACTTCCCATGTTAA 154
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 54930 GCTCACAATGTATCTGTTCATGCTCCCATGTTAA 54898
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14
US-09-803-736-284/c
; Sequence 284, Application US/09803736
; GENERAL INFORMATION:
; APPLICANT: Bush, David F.
; APPLICANT: Levin, Irena M.
; APPLICANT: Norris, Susan R.
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Search completed: May 18, 2004, 20:22:42
Job time : 1681 secs

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RESULT 15
US-09-708-427-21472
; Sequence 21472, Application US/09708427
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: THEREBY
; FILE REFERENCE: 2750-1243P
; CURRENT APPLICATION NUMBER: US/09/708,427
; CURRENT FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 85364
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21472
; LENGTH: 243
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..243
; OTHER INFORMATION: any n = a, g, c, t, unknown, or other
; NAME/KEY: misc feature
; LOCATION: 1..243
; OTHER INFORMATION: Ceres Seq. ID 1839548
US-09-708-427-21472

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Query Match	77.5%;	Score 119.4;	DB 30;	Length 243;
Best Local Similarity	86.3%;	Pred. No. 1.1e-27;		
Matches 132;	Conservative	0;	Mismatches 21;	Indels 0;
Gaps	0;			

QY	2	AGGTTGTGGCAGAGACCAAGTGGGACATGCTAGGAGTTTGTGGGAACAACAATGCGATGC	61
Ddb	91	AAGTTGTGGCAGAGACCAAGTGGTACTTGTGTAGGAGTTTGGGAAACCAACATGGGTGC	150
QY	62	AGGAACCAATGCAGAAACCTTGAAGAGCAGAAACACGGATCTTGCACACTATGCTTCCCA	121
Ddb	151	AAGAATCAGTCGATTAACTTGGGGGGCAACATGGATCTTGCACACTATGCTTCCCA	210
QY	122	GTCACAAATGATTTGTTACTTCCCATGTTAA	154

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 18, 2004, 17:22:46 ; Search time 67.55 Seconds
(without alignments)
2842.409 Million cell updates/sec

Title: US-10-681-972-12_COPY_116_269

Perfect score: 154

Sequence: 1 aaggttgtagagagacaa.....tttgtactcccatgtaa 154

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1745496 seqs, 623391994 residues

Total number of hits satisfying chosen parameters: 3490992

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents NA New.*

- 1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq.*
- 2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
- 3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
- 4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
- 5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
- 6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
- 7: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	35.2	22.9	163548	6	US-10-767-471-10730
C 2	34.6	22.5	42063	6	US-10-417-375A-151
C 3	34.6	22.5	42063	6	US-10-417-375B-151
4	31	20.1	201	7	US-60-568-845-22848
5	31	20.1	201	7	US-60-568-845-22851
6	31	20.1	201	7	US-60-568-845-22854
7	31	20.1	201	7	US-60-568-845-22856
8	31	20.1	201	7	US-60-568-845-22858
9	31	20.1	96902	7	US-60-568-845-22815
10	30.4	19.7	201	7	US-60-568-845-22832
11	30.4	19.7	201	7	US-60-568-845-22842
12	30.4	19.7	201	7	US-60-568-845-22845
C 13	30.4	19.7	1207	1	PCT-US03-41761-31797
C 14	30.4	19.7	1207	1	PCT-US03-41761-31797
15	30	19.5	201	7	US-60-568-845-22830
16	29.8	19.4	76053	6	US-10-767-471-10882
C 17	29.6	19.2	1490	1	PCT-US03-41761-34711
C 18	29.6	19.2	1490	1	PCT-US03-41761-34711
19	29.2	19.0	37544	5	US-09-889-874A-52
20	29	18.8	599	7	US-60-545-213-4176
21	29	18.8	599	7	US-60-545-213-8448
22	28.8	18.7	201	7	US-60-563-440-3885
23	28.8	18.7	201	7	US-60-563-440-21121
C 24	28.8	18.7	2046	1	PCT-US03-41761-48667
C 25	28.8	18.7	2046	1	PCT-US03-41761-48667
26	28.8	18.7	3254	7	US-60-563-440-196

27	28.8	18.7	15254	7	US-60-563-440-11946
C 28	28.6	18.6	35126	6	US-10-796-307-8785
29	28.6	18.6	161065	6	US-10-796-280-12265
C 30	28.6	18.6	161065	6	US-10-796-307-8875
C 31	28.6	18.6	1184710	6	US-10-796-280-12394
C 32	28.6	18.6	1184710	7	US-60-568-845-2921
33	28.4	18.4	201	6	US-10-767-471-25146
34	28.4	18.4	201	6	US-10-796-280-27009
35	28.4	18.4	1331	1	PCT-US04-05654-1590
36	28.4	18.4	261922	6	US-10-767-471-10653
37	28.4	18.4	261922	6	US-10-796-280-12264
C 38	28	18.2	201	7	US-60-568-219-7921
C 39	28	18.2	653	6	US-10-767-701-22795
40	28	18.2	1711	1	PCT-US03-41761-31570
41	28	18.2	1711	1	PCT-US03-41761-31570
42	28	18.2	209822	6	US-10-796-280-12169
43	28	18.2	209822	7	US-60-568-219-6144
C 44	28	18.2	380939	7	US-60-568-219-6153
C 45	27.8	18.1	1663	1	PCT-US03-41761-45120

ALIGNMENTS

RESULT 1

US-10-767-471-10730/c

; Sequence 10730, Application US/10767471

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; FILE REFERENCE: CLO01505

; CURRENT APPLICATION NUMBER: US/10/767,471

; CURRENT FILING DATE: 2004-01-30

; NUMBER OF SEQ ID NOS: 50231

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 10730

; LENGTH: 163548

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)...(163548)

; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-;

US-10-767-471-10730

Query Match

Best Local Similarity 22.9%; Score 35.2; DB 6; Length 163548;

Matches 76; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Qy 3 GGTGTGCGAGAGACCAAGTGGGACATGGTCAGAGTTTGTGGGAACAACAATGCGATGCA 62

Db 157637 GGTGTGCGAGAGACCAAGTGGGACATGGTCAGAGTTTGTGGGAACAACAATGCGATGCA 157578

Qy 63 GGACCAATCAGAAACCTTGAAGACAGACACGATCTTGCACATGCTCTCCAG 122

Db 157577 GGACCAATCAGATAGACTTGTAGTGAAGAAATTCATATTTAAATAATCTTTATTG 157518

Qy 123 CTCACAAATGTTTGTACTTC 146

Db 157517 CTCACCAATGTTTGTACTTC 157494

RESULT 2

US-10-417-375A-151/c

; Sequence 151, Application US/10417375A

; GENERAL INFORMATION:

; APPLICANT: David W. Morris

; APPLICANT: Marc Malandro

; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer

; FILE REFERENCE: 52945201600

; CURRENT APPLICATION NUMBER: US/10/417,375A

; CURRENT FILING DATE: 2003-04-15

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; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 151
; LENGTH: 42063
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(42063)
; OTHER INFORMATION: n = A,T,C or G
US-10-417-375A-151

Query Match      22.5%; Score 34.6; DB 6; Length 42063;
Best Local Similarity 59.8%; Pred. No. 0.26;
Matches 58; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 1 AAGGTGTGCGAGAGACCAATGCGGACATGTCAGGAGTTGTGGGAAACAACAATGATG 60
Db 9183 AAGGCTCAGCTACATACCAAGGCAACCTGTGACGCGGTGTAGTTCCATCAGAGGGTC 9124

QY 61 CAGGAACCAATGCAGAAACCTTGAAAGAGCAGAACAC 97
Db 9123 CAGGCCCTCTGCAGTCACCTGACAAACCCAGGAAC 9087

RESULT 3
US-10-417-375B-151/c
; Sequence 151, Application US/10417375B
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
; FILE REFERENCE: 529452001600
; CURRENT APPLICATION NUMBER: US/10/417,375B
; CURRENT FILING DATE: 2003-04-15
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 151
; LENGTH: 42063
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(42063)
; OTHER INFORMATION: n = A,T,C or G
US-10-417-375B-151

Query Match      22.5%; Score 34.6; DB 6; Length 42063;
Best Local Similarity 59.8%; Pred. No. 0.26;
Matches 58; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 1 AAGGTGTGCGAGAGACCAATGCGGACATGTCAGGAGTTGTGGGAAACAACAATGATG 60
Db 9183 AAGGCTCAGCTACATACCAAGGCAACCTGTGACGCGGTGTAGTTCCATCAGAGGGTC 9124

QY 61 CAGGAACCAATGCAGAAACCTTGAAAGAGCAGAACAC 97
Db 9123 CAGGCCCTCTGCAGTCACCTGACAAACCCAGGAAC 9087

RESULT 4
US-60-568-845-22848
; Sequence 22848, Application US/60568845
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001524
; CURRENT APPLICATION NUMBER: US/60/568,845
; CURRENT FILING DATE: 2004-05-07
; NUMBER OF SEQ ID NOS: 39608
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22848
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-568-845-22848

Query Match      20.1%; Score 31; DB 7; Length 201;
Best Local Similarity 62.0%; Pred. No. 0.51;
Matches 49; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 53 AATGCATGCAGGAACCAATGCAGAAACCTTGAAGAGCAGAACACCGATCTTGCACAT 112
Db 123 AAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAG 181

QY 113 GTCTTCCCAGCTCACAAT 131
Db 182 GACTACTGAGTTGGAAGAT 200

RESULT 5
US-60-568-845-22851
; Sequence 22851, Application US/60568845
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001524
; CURRENT APPLICATION NUMBER: US/60/568,845
; CURRENT FILING DATE: 2004-05-07
; NUMBER OF SEQ ID NOS: 39608
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22851
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-568-845-22851

Query Match      20.1%; Score 31; DB 7; Length 201;
Best Local Similarity 62.0%; Pred. No. 0.51;
Matches 49; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 53 AATGCATGCAGGAACCAATGCAGAAACCTTGAAGAGCAGAACACCGATCTTGCACAT 112
Db 122 AAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAG 181

QY 113 GTCTTCCCAGCTCACAAT 131
Db 182 GACTACTGAGTTGGAAGAT 200

RESULT 6
US-60-568-845-22854
; Sequence 22854, Application US/60568845
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001524
; CURRENT APPLICATION NUMBER: US/60/568,845
; CURRENT FILING DATE: 2004-05-07
; NUMBER OF SEQ ID NOS: 39608
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22854
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-568-845-22854

Query Match      20.1%; Score 31; DB 7; Length 201;
Best Local Similarity 62.0%; Pred. No. 0.51;
Matches 49; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 53 AATGCATGCAGGAACCAATGCAGAAACCTTGAAGAGCAGAACACCGATCTTGCACAT 112
Db 122 AAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAG 181

QY 113 GTCTTCCCAGCTCACAAT 131
Db 182 GACTACTGAGTTGGAAGAT 200
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Db 82 AAGGAAGGAGAAGAAAGAAAAGAAAAAGAGGGAAAAACAGAAAATTCGCACAAT 141
QY 113 GTCTTCCCAGCTCACAAAT 131
 ||| | | | | |
Db 142 GACTACTGAGTTGGAAGAT 160

RESULT 7
US-60-568-845-22856
 ; Sequence 22856, Application US/60568845
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele et al.
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; FILE REFERENCE: CL001524
 ; CURRENT APPLICATION NUMBER: US/60/568,845
 ; CURRENT FILING DATE: 2004-05-07
 ; NUMBER OF SEQ ID NOS: 39608
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 22856
 ; LENGTH: 201
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
US-60-568-845-22856

Query Match 20.1%; Score 31; DB 7; Length 201;
Best Local Similarity 62.0%; Pred. No. 0.51;
Matches 49; Conservative 0; Mismatches 30; Indels 0; Gaps 0

QY 53 AATGCATCAGGAACCATTGCGAATAACCTTGAAAGAGCAGAACACGGATCTTTGCCAACTAT 112
Db 79 AAGGAAGGAAGGAAGGAAGGAAGAAAGAAAGAGGAAACAGAAAATTCGCACAAT 138

QY 113 GTCTTCCAGCTCACAAAT 131
Db 139 GACTACTGAGTTGGAAGAT 157

RESULT 8
US-60-568-845-22858
 ; Sequence 22858, Application US/60568845
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele et al.
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; FILE REFERENCE: CL001524
 ; CURRENT APPLICATION NUMBER: US/60/568,845
 ; CURRENT FILING DATE: 2004-05-07
 ; NUMBER OF SEQ ID NOS: 39608
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 22858
 ; LENGTH: 201
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
US-60-568-845-22858

Query Match 20.1%; Score 31; DB 7; Length 201;
Best Local Similarity 62.0%; Pred. No. 0.51;
Matches 49; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 53 AATGCATCAGGAACCAATGCAGAAACCTTGAAAAGCAGAACACGGATCTTTGCCAACTAT 112
Db 77 AAGGAAGGAAGGAAGGAAGGAAGAAAGAAAGAGGAAACAGAAAATTCGCACAAT 136

QY 113 GTCTTCCCAGCTCACAAAT 131
Db 137 GACTACTGAGTTGGAAGAT 155

RESULT 9
US-60-568-845-2915
 ; Sequence 2915, Application US/60568845
 ; GENERAL INFORMATION:

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 18, 2004, 17:05:11 ; Search time 1282.4 Seconds

(without alignments)

3586.070 Million cell updates/sec

Title: US-10-681-972-12_COPY_116_269

Perfect score: 154

Sequence: 1 aaggttgcgagagaccaa.....ttgttacttccatgttaa 154

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

E8T:*

1: em_estba:**

2: em_estum:**

3: em_estin:**

4: em_estmu:**

5: em_estov:**

6: em_estpl:**

7: em_estro:**

8: em_hcc:**

9: gb_est1:**

10: gb_est2:**

11: gb_hcc:**

12: gb_est3:**

13: gb_est4:**

14: gb_est5:**

15: em_estfun:**

16: em_estom:**

17: em_gss_hum:**

18: em_gss_inv:**

19: em_gss_pln:**

20: em_gss_vrt:**

21: em_gss_fun:**

22: em_gss_mam:**

23: em_gss_mus:**

24: em_gss_pro:**

25: em_gss_rtd:**

26: em_gss_phg:**

27: em_gss_vri:**

28: gb_gse1:**

29: gb_gse2:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	122.6	79.6	418	14	CD832625
2	122.6	79.6	419	14	CD834168
3	122.6	79.6	420	14	CD833944
4	122.6	79.6	421	14	CD826491

5	122.6	79.6	421	14	CD831111
6	122.6	79.6	421	14	CD833977
7	122.6	79.6	422	14	CD831972
8	122.6	79.6	422	14	CD833983
9	122.6	79.6	426	14	CD827413
10	122.6	79.6	438	14	CD831479
11	122.6	79.6	446	14	CD834068
12	122.6	79.6	447	14	CD832592
13	122.6	79.6	452	14	CD832071
14	122.6	79.6	453	14	CD834008
15	122.6	79.6	458	14	CD834994
16	122.6	79.6	470	14	CD831680
17	122.6	79.6	553	14	CD831014
18	122.6	79.6	803	28	BH458392
19	121	78.6	408	14	CD833779
20	121	78.6	409	14	CD834090
21	121	78.6	421	14	CD837517
22	121	78.6	424	14	CD833048
23	121	78.6	438	14	CD831294
24	121	78.6	450	14	CD834611
25	121	78.6	480	14	CD828332
26	119.4	77.5	318	9	AA713157
27	119.4	77.5	394	12	BG321454
28	119.4	77.5	421	9	AV816118
29	119.4	77.5	422	9	AV787956
30	119.4	77.5	441	14	CB263345
31	119.4	77.5	519	14	CD835064
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33	117.8	76.5	344	14	Z29957
34	117.8	76.5	400	14	T04323
35	117.8	76.5	403	14	Z27258
36	117.8	76.5	422	9	AV788559
37	117.8	76.5	422	9	AV789144
38	117.8	76.5	435	14	CB259179
39	113.8	73.9	410	12	BG321515
40	113	73.4	346	14	CA992140
41	113	73.4	457	14	CD831226
42	113	73.4	473	14	CD834995
43	113	73.4	476	14	CD833784
44	113	73.4	476	14	CD834092
45	113	73.4	481	14	CD833924

ALIGNMENTS

RESULT 1
CD832625
LOCUS
DEFINITION
BN40.064A14F011227 BN40 Brassica napus CDNA clone BN40064A14, mRNA
418 bp mRNA linear EST 10-JUL-2003
sequence.
CD832625
CD832625.1 GI:32514565
EST.
SOURCE
Brassica napus (rape)
ORGANISM
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Genoplante.
1 (bases 1 to 418)
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante

Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (<http://www.genoplante.com>) and <http://genoplante-info.infobiogen.fr>.
Location/Qualifiers
1. .418
source


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/organism="Brassica napus"
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/clone="BN40064A14"
/tissue_type="seed"
/clone_lib="BN40"

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Best Local Similarity 87.6%; Pred. No. 6.2e-27;
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 2 AGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAACAACAATGCATGC 61
Db 143 AAGTTGTGCGAGAGGCCAAGTGGGACATGTCAGGAGTCTGTGGAACAACAATGCATGC 202

QY 62 AGGAACCAATGCAGAACCTTGAAGAGCAGAACACGGATCTTGCACATATGTTCCCA 121
Db 203 AAGATCAGTGCATTAACCTTGAGAAAGCAGACATGATCTTGCAACTATGTTCCCA 262

QY 122 GCTCACAATGTATTTGTTACTTCCCATGTTAA 154
Db 263 GCTCACAAGTGTATTTGCTACTTCCCTGTTAA 295

RESULT 2
CD834168
LOCUS
DEFINITION
BN45.040N06F011018 BN45 Brassica napus cDNA clone BN45040N06, mRNA
sequence.
ACCESSION
CD834168
VERSION
CD834168.1 GI:32516108
KEYWORDS
EST.
SOURCE
Brassica napus (rape)
ORGANISM
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 419)
AUTHORS
Genoplante, a major partnership french program in plant genomics
TITLE
Unpublished (2003)
JOURNAL
Contact: Genoplante
COMMENT
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).

FEATURES
Location/Qualifiers
1..419
/organism="Brassica napus"
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/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN45040N06"
/tissue_type="seed"
/clone_lib="BN45"

ORIGIN
Query Match          79.6%; Score 122.6; DB 14; Length 418;
Best Local Similarity 87.6%; Pred. No. 6.2e-27;
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 2 AGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAACAACAATGCATGC 61
Db 140 AAGTTGTGCGAGAGGCCAAGTGGGACATGTCAGGAGTCTGTGGAACAACAATGCATGC 199

QY 62 AGGAACCAATGCAGAACCTTGAAGAGCAGAACACGGATCTTGCACATATGTTCCCA 121
Db 200 AAGATCAGTGCATTAACCTTGAGAAAGCAGACATGATCTTGCAACTATGTTCCCA 259

RESULT 3
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LOCUS
DEFINITION
BN45.040B07F011019 BN45 Brassica napus cDNA clone BN45040B07, mRNA
sequence.
ACCESSION
CD833944
VERSION
CD833944.1 GI:32515884
KEYWORDS
EST.
SOURCE
Brassica napus (rape)
ORGANISM
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 420)
AUTHORS
Genoplante, a major partnership french program in plant genomics
TITLE
Unpublished (2003)
JOURNAL
Contact: Genoplante
COMMENT
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).

FEATURES
Location/Qualifiers
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/organism="Brassica napus"
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Best Local Similarity 87.6%; Pred. No. 6.2e-27;
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 2 AGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAACAACAATGCATGC 61
Db 140 AAGTTGTGCGAGAGGCCAAGTGGGACATGTCAGGAGTCTGTGGAACAACAATGCATGC 199

QY 62 AGGAACCAATGCAGAACCTTGAAGAGCAGAACACGGATCTTGCACATATGTTCCCA 121
Db 200 AAGATCAGTGCATTAACCTTGAGAAAGCAGACATGATCTTGCAACTATGTTCCCA 259

RESULT 4
CD826491
LOCUS
DEFINITION
BN25.064A05F020416 BN25 Brassica napus cDNA clone BN25064A05, mRNA
sequence.
ACCESSION
CD826491
VERSION
CD826491.1 GI:32508431
KEYWORDS
EST.
SOURCE
Brassica napus (rape)
ORGANISM
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 421)

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QY 122 GCTCACAATGTATTTGTTACTTCCCATGTTAA 154
Db 260 GCTCACAAGTGTATTTGCTACTTCCCTGTTAA 292

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RESULT 3
CD833944
LOCUS
DEFINITION
BN45.040B07F011019 BN45 Brassica napus cDNA clone BN45040B07, mRNA
sequence.
ACCESSION
CD833944
VERSION
CD833944.1 GI:32515884
KEYWORDS
EST.
SOURCE
Brassica napus (rape)
ORGANISM
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 420)
AUTHORS
Genoplante, a major partnership french program in plant genomics
TITLE
Unpublished (2003)
JOURNAL
Contact: Genoplante
COMMENT
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).

FEATURES
Location/Qualifiers
1..420
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN45040B07"
/tissue_type="seed"
/clone_lib="BN45"

ORIGIN
Query Match          79.6%; Score 122.6; DB 14; Length 420;
Best Local Similarity 87.6%; Pred. No. 6.2e-27;
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 2 AGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGAACAACAATGCATGC 61
Db 140 AAGTTGTGCGAGAGGCCAAGTGGGACATGTCAGGAGTCTGTGGAACAACAATGCATGC 199

QY 62 AGGAACCAATGCAGAACCTTGAAGAGCAGAACACGGATCTTGCACATATGTTCCCA 121
Db 200 AAGATCAGTGCATTAACCTTGAGAAAGCAGACATGATCTTGCAACTATGTTCCCA 259

RESULT 4
CD826491
LOCUS
DEFINITION
BN25.064A05F020416 BN25 Brassica napus cDNA clone BN25064A05, mRNA
sequence.
ACCESSION
CD826491
VERSION
CD826491.1 GI:32508431
KEYWORDS
EST.
SOURCE
Brassica napus (rape)
ORGANISM
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 421)

```

AUTHORS
TITLE Genoplante, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplante
 Genoplante
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10
 This sequence has been generated in the framework of the french
 plant genomics programme 'Genoplante' (<http://www.genoplante.com>
 and <http://genoplante-info.infobiogen.fr>).

FEATURES
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 Location/Qualifiers
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 Best Local Similarity 87.6%; Pred. No. 6.2e-27;
 Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
 QY 2 AGGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTGTGGGAACAACAATGCATGC 61
 Db 141 AAGTTGTGCGAGAGGCCAAGTGGGACATGTCAGGAGTCTGTGGAAACAATAACGCATGC 200
 QY 62 AGGAACAATGCAGAACCTTGAAGAGCAGACACGAGATCTTGCACACTATGTCTTCCCA 121
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 QY 122 GCTCACAAGTATTTGCTACTTCCCTTTGTTAA 154
 Db 261 GCTCACAAGTATTTGCTACTTCCCTTTGTTAA 293

RESULT 5
CD831111
LOCUS 421 bp mRNA linear EST 10-JUL-2003
DEFINITION BN40.058A09F011019 BN40 Brassica napus cDNA clone BN40058A09, mRNA
 sequence.
ACCESSION CD831111
VERSION CD831111.1 GI:32513051
KEYWORDS EST.
SOURCE Brassica napus (rape)
ORGANISM Brassica napus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 421)
 Genoplante.
REFERENCE
AUTHORS Genoplante, a major partnership french program in plant genomics
TITLE Unpublished (2003)
JOURNAL Contact: Genoplante
COMMENT Genoplante
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10
 This sequence has been generated in the framework of the french
 plant genomics programme 'Genoplante' (<http://www.genoplante.com>
 and <http://genoplante-info.infobiogen.fr>).

FEATURES
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 Location/Qualifiers
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 /mol_type="mRNA"
 /cultivar="Jet neuf"
 /db_xref="taxon:3708"
 /clone="BN40058A09"
 /tissue_type="seed"
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Query Match 79.6%; Score 122.6; DB 14; Length 421;
 Best Local Similarity 87.6%; Pred. No. 6.2e-27;
 Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
 QY 2 AGGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTGTGGGAACAACAATGCATGC 61
 Db 141 AAGTTGTGCGAGAGGCCAAGTGGGACATGTCAGGAGTCTGTGGAAACAATAACGCATGC 200
 QY 62 AGGAACAATGCAGAACCTTGAAGAGCAGACACGAGATCTTGCACACTATGTCTTCCCA 121
 Db 201 AAGAATCAGTGCATTAACCTTGAAGAAAGCAGACATGTAATGTCACACTATGTCTTCCCA 260
 QY 122 GCTCACAAGTATTTGCTACTTCCCTTTGTTAA 154
 Db 261 GCTCACAAGTATTTGCTACTTCCCTTTGTTAA 293

RESULT 6
CD833977
LOCUS 421 bp mRNA linear EST 10-JUL-2003
DEFINITION BN45.040D05F011019 BN45 Brassica napus cDNA clone BN45040D05, mRNA
 sequence.
ACCESSION CD833977
VERSION CD833977.1 GI:32515917
KEYWORDS EST.
SOURCE Brassica napus (rape)
ORGANISM Brassica napus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 421)
 Genoplante.
REFERENCE
AUTHORS Genoplante, a major partnership french program in plant genomics
TITLE Unpublished (2003)
JOURNAL Contact: Genoplante
COMMENT Genoplante
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10
 This sequence has been generated in the framework of the french
 plant genomics programme 'Genoplante' (<http://www.genoplante.com>
 and <http://genoplante-info.infobiogen.fr>).

FEATURES
 source
 Location/Qualifiers
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ORIGIN

Query Match 79.6%; Score 122.6; DB 14; Length 421;
 Best Local Similarity 87.6%; Pred. No. 6.2e-27;
 Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
 QY 2 AGGTTGTGCGAGAGACCAAGTGGGACATGTCAGGAGTTGTGGGAACAACAATGCATGC 61
 Db 141 AAGTTGTGCGAGAGGCCAAGTGGGACATGTCAGGAGTCTGTGGAAACAATAACGCATGC 200
 QY 62 AGGAACAATGCAGAACCTTGAAGAGCAGACACGAGATCTTGCACACTATGTCTTCCCA 121
 Db 201 AAGAATCAGTGCATTAACCTTGAAGAAAGCAGACATGTAATGTCACACTATGTCTTCCCA 260
 QY 122 GCTCACAAGTATTTGCTACTTCCCTTTGTTAA 154
 Db 261 GCTCACAAGTATTTGCTACTTCCCTTTGTTAA 293

RESULT 7

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CD831972
LOCUS
DEFINITION
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ACCESSION
  CD831972
KEYWORDS
  CD831972.1 GI:32513912
SOURCE
  Brassica napus (rape)
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
  1 (bases 1 to 422)
AUTHORS
  Genoplante.
TITLE
  Genoplante, a major partnership french program in plant genomics
JOURNAL
  Unpublished (2003)
COMMENT
  Contact: Genoplante
  Genoplante
  93, rue Henri Rochefort 91025 EVRY CEDEX France
  Tel: 33 1 69 47 54 00
  Fax: 33 1 69 47 54 10
  This sequence has been generated in the framework of the french
  plant genomics programme 'Genoplante' (http://www.genoplante.com
  and http://genoplante-info.infobiogen.fr).

FEATURES
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    /organism="Brassica napus"
    /mol_type="mRNA"
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    /clone_lib="BN40"

ORIGIN
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  Best Local Similarity 87.6%; Pred. No. 6.2e-27;
  Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

  QY 2 AGTTGTGGGAGAGACCAAGTGGGACATGTCAGGAGTTGTGGGAACAACATGATGC 61
  DB 141 AAGTTGTGGGAGAGCCAAAGTGGGACATGTCAGGAGTTGTGGGAACAACATGATGC 200

  QY 62 AGAACCAATGCAAAACCTTGAAGAGCAGAACACGAGATCTTGCAACTATGTTCTCCCA 121
  DB 201 AAGATCACTGATTAACCTTGAGAAAGCAGACATGATCTTGCAACTATGTTCTCCCA 260

  QY 122 GCTCAAAATGATTTGTTACTTCCCATGTTAA 154
  DB 261 GCTCAAGTGTATTGCTACTTCCCTTGTAA 293

  RESULT 8
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  DEFINITION
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  VERSION
    CD827413.1 GI:32509353
  KEYWORDS
    EST.
  SOURCE
    Brassica napus (rape)
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
    rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
  REFERENCE
    1 (bases 1 to 426)
  AUTHORS
    Genoplante.
  TITLE
    Genoplante, a major partnership french program in plant genomics
  JOURNAL
    Unpublished (2003)
  COMMENT
    Contact: Genoplante
    Genoplante
    93, rue Henri Rochefort 91025 EVRY CEDEX France
    Tel: 33 1 69 47 54 00
    Fax: 33 1 69 47 54 10
    This sequence has been generated in the framework of the french
    plant genomics programme 'Genoplante' (http://www.genoplante.com
    and http://genoplante-info.infobiogen.fr).

FEATURES
  source
    1..426
    /organism="Brassica napus"
    /mol_type="mRNA"
    /cultivar="Jet neuf"
    /db_xref="taxon:3708"
    /clone="BN25067G02"
    /tissue_type="seed"
    /clone_lib="BN25"

ORIGIN
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  Best Local Similarity 87.6%; Pred. No. 6.2e-27;
  Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

  QY 2 AGTTGTGGGAGAGACCAAGTGGGACATGTCAGGAGTTGTGGGAACAACATGATGC 61
  DB 141 AAGTTGTGGGAGAGCCAAAGTGGGACATGTCAGGAGTTGTGGGAACAACATGATGC 200

  QY 62 AGAACCAATGCAAAACCTTGAAGAGCAGAACACGAGATCTTGCAACTATGTTCTCCCA 121
  DB 201 AAGATCACTGATTAACCTTGAGAAAGCAGACATGATCTTGCAACTATGTTCTCCCA 260

  QY 122 GCTCAAAATGATTTGTTACTTCCCATGTTAA 154
  DB 261 GCTCAAGTGTATTGCTACTTCCCTTGTAA 293

  RESULT 8
  LOCUS
  DEFINITION
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    sequence.
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  VERSION
    CD833983.1 GI:32515923
  KEYWORDS
    EST.
  SOURCE
    Brassica napus (rape)
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
    rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
  REFERENCE
    1 (bases 1 to 422)
  AUTHORS
    Genoplante.
  TITLE
    Genoplante, a major partnership french program in plant genomics
  JOURNAL
    Unpublished (2003)
  COMMENT
    Contact: Genoplante
    Genoplante
    93, rue Henri Rochefort 91025 EVRY CEDEX France
    Tel: 33 1 69 47 54 00

```

```

Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).

FEATURES
  source
    1..422
    /organism="Brassica napus"
    /mol_type="mRNA"
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    /db_xref="taxon:3708"
    /clone="BN45040D11"
    /tissue_type="seed"
    /clone_lib="BN45"

ORIGIN
  Query Match 79.6%; Score 122.6; DB 14; Length 422;
  Best Local Similarity 87.6%; Pred. No. 6.2e-27;
  Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

  QY 2 AGTTGTGGGAGAGACCAAGTGGGACATGTCAGGAGTTGTGGGAACAACATGATGC 61
  DB 141 AAGTTGTGGGAGAGCCAAAGTGGGACATGTCAGGAGTTGTGGGAACAACATGATGC 200

  QY 62 AGAACCAATGCAAAACCTTGAAGAGCAGAACACGAGATCTTGCAACTATGTTCTCCCA 121
  DB 201 AAGATCACTGATTAACCTTGAGAAAGCAGACATGATCTTGCAACTATGTTCTCCCA 260

  QY 122 GCTCAAAATGATTTGTTACTTCCCATGTTAA 154
  DB 261 GCTCAAGTGTATTGCTACTTCCCTTGTAA 293

  RESULT 9
  LOCUS
  DEFINITION
    BN25.067G02F020123 BN25 Brassica napus cDNA clone BN25067G02, mRNA
    sequence.
  ACCESSION
    CD827413
  VERSION
    CD827413.1 GI:32509353
  KEYWORDS
    EST.
  SOURCE
    Brassica napus (rape)
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
    rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
  REFERENCE
    1 (bases 1 to 426)
  AUTHORS
    Genoplante.
  TITLE
    Genoplante, a major partnership french program in plant genomics
  JOURNAL
    Unpublished (2003)
  COMMENT
    Contact: Genoplante
    Genoplante
    93, rue Henri Rochefort 91025 EVRY CEDEX France
    Tel: 33 1 69 47 54 00
    Fax: 33 1 69 47 54 10
    This sequence has been generated in the framework of the french
    plant genomics programme 'Genoplante' (http://www.genoplante.com
    and http://genoplante-info.infobiogen.fr).

FEATURES
  source
    1..426
    /organism="Brassica napus"
    /mol_type="mRNA"
    /cultivar="Jet neuf"
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    /tissue_type="seed"
    /clone_lib="BN25"

ORIGIN
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  Best Local Similarity 87.6%; Pred. No. 6.2e-27;
  Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

  QY 2 AGTTGTGGGAGAGACCAAGTGGGACATGTCAGGAGTTGTGGGAACAACATGATGC 61

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141 AGTTGTGGGAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC 200
62 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGAGATCTTGCAACTATGCTTCCCA 121
201 AAGATCAGTGCATTAACCTTGAGAAAGCAGACATGATCTTGCAACTATGCTTCCCA 260
122 GCTCAAAATGATTTGTTACTTCCCATGTTAA 154
261 GCTCAAAAGTGTATTGCTACTTCCCTTGTTAA 293

RESULT 10
CD831479
LOCUS
DEFINITION BN40.059J13F011208 BN40 Brassica napus cDNA clone BN40059J13, mRNA
sequence.
ACCESSION CD831479
VERSION
KEYWORDS
SOURCE
ORGANISM Brassica napus (rape)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 438)
Genoplatte, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplatte
Genoplatte
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplatte' (http://www.genoplatte.com)
and http://genoplatte-info.infobiogen.fr.

FEATURES
source
location/Qualifiers
1..438
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN40059J13"
/tissue_type="seed"
/clone_lib="BN40"

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Best Local Similarity 87.6%; Pred. No. 6.2e-27;
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 2 AGTTGTGGGAGACCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC 61
Db 156 AAGTTGTGGGAGAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC 215
QY 62 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGAGATCTTGCAACTATGCTTCCCA 121
Db 216 AAGATCAGTGCATTAACCTTGAGAAAGCAGACATGATCTTGCAACTATGCTTCCCA 275
QY 122 GCTCAAAATGATTTGTTACTTCCCATGTTAA 154
Db 276 GCTCAAAAGTGTATTGCTACTTCCCTTGTTAA 308

RESULT 12
CD832592
LOCUS
DEFINITION BN40.063O15F011228 BN40 Brassica napus cDNA clone BN40063O15, mRNA
sequence.
ACCESSION CD832592
VERSION
KEYWORDS
SOURCE
ORGANISM Brassica napus (rape)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 447)
Genoplatte, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplatte
Genoplatte
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplatte' (http://www.genoplatte.com)
and http://genoplatte-info.infobiogen.fr.

FEATURES
source
location/Qualifiers
1..447
/organism="Brassica napus"

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SOURCE
ORGANISM Brassica napus (rape)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 446)
Genoplatte, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplatte
Genoplatte
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplatte' (http://www.genoplatte.com)
and http://www.genoplatte.com.

FEATURES
source
location/Qualifiers
1..446
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN45040H17"
/tissue_type="seed"
/clone_lib="BN45"

ORIGIN
Query Match 79.6%; Score 122.6; DB 14; Length 446;
Best Local Similarity 87.6%; Pred. No. 6.3e-27;
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 2 AGTTGTGGGAGACCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC 61
Db 156 AAGTTGTGGGAGAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC 215
QY 62 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGAGATCTTGCAACTATGCTTCCCA 121
Db 216 AAGATCAGTGCATTAACCTTGAGAAAGCAGACATGATCTTGCAACTATGCTTCCCA 275
QY 122 GCTCAAAATGATTTGTTACTTCCCATGTTAA 154
Db 276 GCTCAAAAGTGTATTGCTACTTCCCTTGTTAA 308

RESULT 12
CD832592
LOCUS
DEFINITION BN40.063O15F011228 BN40 Brassica napus cDNA clone BN40063O15, mRNA
sequence.
ACCESSION CD832592
VERSION
KEYWORDS
SOURCE
ORGANISM Brassica napus (rape)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 447)
Genoplatte, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplatte
Genoplatte
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplatte' (http://www.genoplatte.com)
and http://www.genoplatte.com.

FEATURES
source
location/Qualifiers
1..447
/organism="Brassica napus"

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RESULT 11
CD834068
LOCUS
DEFINITION BN45.040H17F011019 BN45 Brassica napus cDNA clone BN45040H17, mRNA
sequence.
ACCESSION CD834068
VERSION
KEYWORDS
EST.

CD834068
LOCUS
DEFINITION BN45.040H17F011019 BN45 Brassica napus cDNA clone BN45040H17, mRNA
sequence.
ACCESSION CD834068
VERSION
KEYWORDS
EST.

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/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN40061003"
/tissue_type="seed"
/clone_lib="BN40"

ORIGIN
Query Match          79.6%; Score 122.6; DB 14; Length 447;
Best Local Similarity 87.6%; Pred. No. 6.3e-27;
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY  2 AGTTGTGCGAGAGACCAAGTGGGACATGTCAGAGTTTGTGGGAACAACATGCATGC 61
Db  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY  62 AGGAACCAATGCAGAAACCTTGAAGAGACGACACACGATCTTCAACTATGCTTCCCA 121
Db  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY  215 AAGAATCAGTGCATTAACCTTGAGAAAGCAGCATGATCTTCAACTATGCTTCCCA 274
Db  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY  122 GCTCACAATGTATTGTTACTTCCCATGTTAA 154
Db  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY  275 GCTCACAAGTGTATTGCTACTTCCCTGTTAA 307
Db  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 13
LOCUS CD832071 452 bp mRNA linear EST 10-JUL-2003
DEFINITION BN40.061003F011227 BN40 Brassica napus cDNA clone BN40061003, mRNA
sequence.
ACCESSION CD832071
VERSION CD832071.1 GI:32514011
KEYWORDS EST.
SOURCE Brassica napus (rape)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 452)
AUTHORS Genoplante.
TITLE Genoplante, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).

FEATURES
source
1..452
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN40061003"
/tissue_type="seed"
/clone_lib="BN40"

ORIGIN
Query Match          79.6%; Score 122.6; DB 14; Length 452;
Best Local Similarity 87.6%; Pred. No. 6.3e-27;
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY  2 AGTTGTGCGAGAGACCAAGTGGGACATGTCAGAGTTTGTGGGAACAACATGCATGC 61
Db  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY  160 AAGTTGTGCGAGAGGCCAAGTGGGACATGTCAGAGTCTGTGGAAACAATACCATGC 219
Db  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY  62 AGGAACCAATGCAGAAACCTTGAAGAGACGACACGATCTTCAACTATGCTTCCCA 121
Db  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY  220 AAGAATCAGTGCATTAACCTTGAGAAAGCAGCATGATCTTCAACTATGCTTCCCA 279
Db  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 14
LOCUS CD834008 453 bp mRNA linear EST 10-JUL-2003
DEFINITION BN45.040618F011019 BN45 Brassica napus cDNA clone BN45040618, mRNA
sequence.
ACCESSION CD834008
VERSION CD834008.1 GI:32515948
KEYWORDS EST.
SOURCE Brassica napus (rape)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 453)
AUTHORS Genoplante.
TITLE Genoplante, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).

FEATURES
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/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN45040618"
/tissue_type="seed"
/clone_lib="BN45"

ORIGIN
Query Match          79.6%; Score 122.6; DB 14; Length 453;
Best Local Similarity 87.6%; Pred. No. 6.3e-27;
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY  2 AGTTGTGCGAGAGACCAAGTGGGACATGTCAGAGTTTGTGGGAACAACATGCATGC 61
Db  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY  141 AAGTTGTGCGAGAGGCCAAGTGGGACATGTCAGAGTCTGTGGAAACAATACCATGC 200
Db  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY  62 AGGAACCAATGCAGAAACCTTGAAGAGACGACACGATCTTCAACTATGCTTCCCA 121
Db  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY  201 AAGAATCAGTGCATTAACCTTGAGAAAGCAGCATGATCTTCAACTATGCTTCCCA 260
Db  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY  122 GCTCACAATGTATTGTTACTTCCCATGTTAA 154
Db  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY  261 GCTCACAAGTGTATTGCTACTTCCCTGTTAA 293
Db  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 15
LOCUS CD834994 458 bp mRNA linear EST 10-JUL-2003
DEFINITION BN45.043006F011229 BN45 Brassica napus cDNA clone BN45043006, mRNA
sequence.
ACCESSION CD834994
VERSION CD834994.1 GI:32516934
KEYWORDS EST.
SOURCE Brassica napus (rape)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 458)
AUTHORS Genoplante.

```

TITLE Genoplante, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (<http://www.genoplante.com>)
and <http://genoplante-info.infobiogen.fr>.

FEATURES

source
1..458
Location/Qualifiers
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN45043006"
/tissue_type="seed"
/clone_id="BN45"

ORIGIN

Query Match 79.6%; Score 122.6; DB 14; Length 458;
Best Local Similarity 87.6%; Pred. No. 6.3e-27;
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
Qy 2 AGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGGGAAACAACAATGCATGC 61
Db 156 AAGTTGTGCGAGAGAGCCAAAGTGGGACATGGTCAGGAGTCTGTGGAACAATAACGCATGC 215
Qy 62 AGGAACCAATGCAGAAACCTTGAAGAGACAGACACGGATCTTGCACATATGTCTTCCCA 121
Db 216 AAGAATCAGTGCATTAACCTTGAGAAAGCAGCATGGATCTTGCACATATGTCTTCCCA 275
Qy 122 GCTCACAATGATTTGTTACTTCCCATGTTAA 154
Db 276 GCTCACAAGTGATTTGCTACTTCCCTTGTTAA 308

Search completed: May 18, 2004, 19:00:30
Job time : 1283.4 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 18, 2004, 19:02:23 ; Search time 2171 Seconds
(without alignments)
998.227 Million cell updates/sec

Title: US-10-681-972-2

Perfect score: 305
Sequence: 1 RLCERPSTGWSGVCGNNAC.....EHGSCNVVFAHKICICYFPC 50

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
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Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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40: em.htgo.mus.*
41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Query Length	DB ID	Description
1	305	100.0	270	6	AR014691 Sequence
2	305	100.0	270	6	AR432391 Sequence
3	305	100.0	286	6	AR014689 Sequence
4	305	100.0	286	6	AR432389 Sequence
5	296	97.0	500	6	AR014686 Sequence
6	296	97.0	500	6	AR432386 Sequence
7	283	92.8	285	6	AR014692 Sequence
8	283	92.8	285	6	AR432392 Sequence
9	283	92.8	395	8	RSU18557
10	283	92.8	414	6	A26875
11	283	92.8	414	6	A39549
12	283	92.8	414	6	A63404
13	283	92.8	414	6	AR050153
14	283	92.8	414	6	AR130272
15	283	92.8	414	6	I23728
16	283	92.8	414	6	AR207337
17	283	92.8	414	6	AR374914
18	278	91.1	243	6	AX412406
19	278	91.1	243	6	AX412601
20	278	91.1	243	6	AX651878
21	278	91.1	243	8	AY060506
22	278	91.1	403	6	A68645
23	278	91.1	403	8	ATANTSPEC
24	278	91.1	425	8	AY052236
25	278	91.1	471	11	BV010672
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32	277	90.8	933	8	BOL311046
33	274	89.8	285	6	AR014693
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35	274	89.8	288	6	A39553
36	274	89.8	288	6	AR050161
37	274	89.8	288	6	AR130280
38	274	89.8	288	6	I23736
39	274	89.8	449	6	E34290
40	274	89.8	457	8	RSU18556
41	274	89.8	522	6	BD223233
42	274	89.8	534	6	BD240936
43	274	89.8	534	6	BD223234
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ALIGNMENTS

RESULT 1

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LOCUS AR014691 270 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 14 from patent US 5773696.
ACCESSION AR014691
VERSION AR014691.1 GI:3972145
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 270)
AUTHORS Liang, J., Shah, D.M., Wu, Y.S., and Rosenberger, C.A.
TITLE Antifungal polypeptide and methods for controlling plant pathogenic fungi
JOURNAL Patent: US 5773696-A 14 30-JUN-1998;
FEATURES
    Location/Qualifiers
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    /organism="unknown"
    /mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 3.38e-27 Length: 270
Score: 305.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-681-972-2 (1-50) x AR014691 (1-270)
QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 109 AGTTGTGCGAGAGACCAAGTGGACATGCTCAGGAGTTTGTGGGAACAACATGTCATGC 168
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 169 AGAACCAATGCAGAACCTTGAAGAGCAGAACACGGATCTTGCAACTATGCTTCCCA 228
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 229 GCTCACAAATGTTTGTACTTCCCATGT 258
RESULT 2
LOCUS AR014691 270 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 14 from patent US 6653280.
ACCESSION AR014691
VERSION AR014691.1 GI:40194668
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 270)
AUTHORS Liang, J., Shah, D.M., Wu, Y.S., and Rosenberger, C.A.
TITLE Antifungal polypeptide AlyAPP from Alyssum and methods for controlling plant pathogenic fungi
JOURNAL Patent: US 6653280-A 14 25-NOV-2003;
FEATURES
    Location/Qualifiers
    1..270
    /organism="unknown"
    /mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 3.38e-27 Length: 270
Score: 305.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-681-972-2 (1-50) x AR014691 (1-270)
QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 109 AGTTGTGCGAGAGACCAAGTGGACATGCTCAGGAGTTTGTGGGAACAACATGTCATGC 168
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 169 AGAACCAATGCAGAACCTTGAAGAGCAGAACACGGATCTTGCAACTATGCTTCCCA 228
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 229 GCTCACAAATGTTTGTACTTCCCATGT 258
RESULT 2
LOCUS AR014691 270 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 14 from patent US 6653280.
ACCESSION AR014691
VERSION AR014691.1 GI:40194668
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 270)
AUTHORS Liang, J., Shah, D.M., Wu, Y.S., and Rosenberger, C.A.
TITLE Antifungal polypeptide AlyAPP from Alyssum and methods for controlling plant pathogenic fungi
JOURNAL Patent: US 6653280-A 14 25-NOV-2003;
FEATURES
    Location/Qualifiers
    1..270
    /organism="unknown"
    /mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 3.38e-27 Length: 270
Score: 305.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-681-972-2 (1-50) x AR014691 (1-270)
QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 109 AGTTGTGCGAGAGACCAAGTGGACATGCTCAGGAGTTTGTGGGAACAACATGTCATGC 168
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 169 AGAACCAATGCAGAACCTTGAAGAGCAGAACACGGATCTTGCAACTATGCTTCCCA 228
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 229 GCTCACAAATGTTTGTACTTCCCATGT 258

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QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 109 AGTTGTGCGAGAGACCAAGTGGACATGCTCAGGAGTTTGTGGGAACAACATGTCATGC 168
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 169 AGAACCAATGCAGAACCTTGAAGAGCAGAACACGGATCTTGCAACTATGCTTCCCA 228
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 229 GCTCACAAATGTTTGTACTTCCCATGT 258
RESULT 3
LOCUS AR014689 286 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 12 from patent US 5773696.
ACCESSION AR014689
VERSION AR014689.1 GI:3972143
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 286)
AUTHORS Liang, J., Shah, D.M., Wu, Y.S., and Rosenberger, C.A.
TITLE Antifungal polypeptide and methods for controlling plant pathogenic fungi
JOURNAL Patent: US 5773696-A 12 30-JUN-1998;
FEATURES
    Location/Qualifiers
    1..286
    /organism="unknown"
    /mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 3.61e-27 Length: 286
Score: 305.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-681-972-2 (1-50) x AR014689 (1-286)
QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 117 AGTTGTGCGAGAGACCAAGTGGACATGCTCAGGAGTTTGTGGGAACAACATGTCATGC 176
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 177 AGAACCAATGCAGAACCTTGAAGAGCAGAACACGGATCTTGCAACTATGCTTCCCA 236
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 237 GCTCACAAATGTTTGTACTTCCCATGT 266
RESULT 4
LOCUS AR432389 286 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 12 from patent US 6653280.
ACCESSION AR432389
VERSION AR432389.1 GI:40194666
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 286)
AUTHORS Liang, J., Shah, D.M., Wu, Y.S., and Rosenberger, C.A.
TITLE Antifungal polypeptide AlyAPP from Alyssum and methods for controlling plant pathogenic fungi
JOURNAL Patent: US 6653280-A 12 25-NOV-2003;
FEATURES
    Location/Qualifiers
    1..286
    /organism="unknown"

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/mol_type="genomic DNA"

ORIGIN

Alignment Scores:

Pred. No.: 3 61e-27 Length: 286
Score: 305.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-681-972-2 (1-50) x AR432389 (1-286)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 117 AGGTTGTGCGAGACCAAGTGGGACATGTTGAGGATTTGGGAAACAACATGCATGC 176
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 177 AGGAACCAATGCAGAAACCTTGAAGAGCAGAACACCGATCTTGCAACTATGTCTTCCCA 236
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 237 GCTCACAAATGTATTGTACTTCCCATGT 266

RESULT 5

AR014686
LOCUS AR014686 500 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 9 from patent US 5773696.
ACCESSION AR014686
VERSION AR014686.1 GI:3972140
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 500)
AUTHORS Liang,J., Shah,D.Maganlal., Wu,Y.Shun. and Rosenberger,C.Annette.
TITLE Antifungal polypeptide and methods for controlling plant pathogenic fungi
JOURNAL Patent: US 5773696-A 9 30-JUN-1998;
FEATURES Location/Qualifiers
source 1..500
/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 7.95e-26 Length: 500
Score: 296.00 Matches: 48
Percent Similarity: 98.00% Conservative: 1
Best Local Similarity: 96.00% Mismatches: 1
Query Match: 97.05% Indels: 0
DB: 6 Gaps: 0

US-10-681-972-2 (1-50) x AR014686 (1-500)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 159 AAGTTGTGCGAGAGTCCAAAGTGAACATGTTGAGGATTTGGGAAATAAATACGCATGC 218
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 219 AGGAACCAATGCAGAAACCTTGAAGAGCAGAACACCGATCTTGCAACTATGTCTTCCCA 278
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 279 GCTCACAAATGTATTGTACTTCCCATGT 308

RESULT 6

AR432386
LOCUS AR432386 500 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 9 from patent US 6653280.
ACCESSION AR432386

VERSION AR432386.1 GI:40194663

KEYWORDS

SOURCE Unknown.

ORGANISM

Unknown.

REFERENCE

1 (bases 1 to 500)
AUTHORS Liang,J., Shah,D.M., Wu,Y.S. and Rosenberger,C.A.
TITLE Antifungal polypeptide AlyAFP from Alyssum and methods for controlling plant pathogenic fungi
JOURNAL Patent: US 6653280-A 9 25-NOV-2003;
FEATURES Location/Qualifiers
source 1..500
/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Alignment Scores:

Pred. No.: 7.95e-26 Length: 500
Score: 296.00 Matches: 48
Percent Similarity: 98.00% Conservative: 1
Best Local Similarity: 96.00% Mismatches: 1
Query Match: 97.05% Indels: 0
DB: 6 Gaps: 0

US-10-681-972-2 (1-50) x AR432386 (1-500)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 159 AAGTTGTGCGAGAGTCCAAAGTGAACATGTTGAGGATTTGGGAAATAAATACGCATGC 218
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 219 AGGAACCAATGCAGAAACCTTGAAGAGCAGAACACCGATCTTGCAACTATGTCTTCCCA 278
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 279 GCTCACAAATGTATTGTACTTCCCATGT 308

RESULT 7

AR014692
LOCUS AR014692 285 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 16 from patent US 5773696.
ACCESSION AR014692
VERSION AR014692.1 GI:3972146
KEYWORDS
SOURCE Unknown.

ORGANISM

Unknown.

REFERENCE

1 (bases 1 to 285)
AUTHORS Liang,J., Shah,D.Maganlal., Wu,Y.Shun. and Rosenberger,C.Annette.
TITLE Antifungal polypeptide and methods for controlling plant pathogenic fungi
JOURNAL Patent: US 5773696-A 16 30-JUN-1998;
FEATURES Location/Qualifiers
source 1..285
/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 1.42e-24 Length: 285
Score: 283.00 Matches: 45
Percent Similarity: 96.00% Conservative: 3
Best Local Similarity: 90.00% Mismatches: 2
Query Match: 92.79% Indels: 0
DB: 6 Gaps: 0

US-10-681-972-2 (1-50) x AR014692 (1-285)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 121 AAGTTGTGCGAGAGGCCATCAGGACTTGGTCAGGAGTCTGCGGAAACAACACGCATGC 180

QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
 Db 181 AAGAACCAATGATCAACCTCGAGAGGCGGCGATGATCTGCACTAGCTTCCCA 240
 QY 41 AlaHisLysCysIleCysTyrPheProCys 50
 Db 241 GCTCAAGTGCATCTGCTACTTTCCATGC 270

RESULT 8
 AR432392
 LOCUS
 DEFINITION Sequence 16 from patent US 6653280.
 ACCESSION AR432392
 VERSION AR432392.1 GI:40194669
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.
 REFERENCE 1. (bases 1 to 285)
 AUTHORS Liang,J., Shah,D.M., Wu,Y.S. and Rosenberger,C.A.
 TITLE Antifungal polypeptide AlyAPP from *Alyssum* and methods for
 controlling plant pathogenic fungi
 JOURNAL Patent: US 6653280-A 16 25-NOV-2003;
 FEATURES Location/Qualifiers
 source
 1..285
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN
 Alignment Scores:
 Pred. No.: 1.42e-24 Length: 285
 Score: 283.00 Matches: 45
 Percent Similarity: 96.00% Conservative: 3
 Best Local Similarity: 90.00% Mismatches: 2
 Query Match: 92.79% Indels: 0
 DB: 6 Gaps: 0

US-10-681-972-2 (1-50) x AR432392 (1-285)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
 Db 121 AAGTTGGCGAGGCGCATCAGGACTTGTCTAGGAGTCTGCGGAACACCAACGCGATGC 180
 QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
 Db 181 AAGAACCAATGATCAACCTCGAGAGGCGGCGATGATCTGCACTAGCTTCCCA 240
 QY 41 AlaHisLysCysIleCysTyrPheProCys 50
 Db 241 GCTCAAGTGCATCTGCTACTTTCCATGC 270

RESULT 9
 RSU18557
 LOCUS
 DEFINITION Raphanus sativus antifungal protein 1 preprotein (Rs-APP1) mRNA,
 complete cds.
 ACCESSION U18557
 VERSION U18557.1 GI:644773
 KEYWORDS
 SOURCE Raphanus sativus (radish)
 ORGANISM Raphanus sativus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Raphanus.
 REFERENCE 1. (sites)
 AUTHORS Terras,F.R.G., Eggermont,K., Kovaleva,V., Raikhel,N.V.,
 Osborn,R.W., Kester,A., Rees,S.B., Torrekens,S., Van Leuven,F.,
 Vanderleyden,J., Cammue,B.P.A. and Broekaert,W.F.
 TITLE Small cysteine-rich antifungal proteins from radish: their role in
 host defense
 JOURNAL Plant Cell 7, 568-573 (1995)
 REFERENCE 2. (bases 1 to 395)
 AUTHORS Terras,F.R.

TITLE Direct Submission
 JOURNAL Submitted (14-DEC-1994) Franky R. Terras, F.A. Janssens Laboratory
 of Genetics, Applied Biological Sciences, W. De Croylaan 42,
 Heverlee, Belgium, B-3001
 COMMENT On Feb 9, 1995 this sequence version replaced gi:609321.
 FEATURES Location/Qualifiers
 source
 1..395
 /organism="Raphanus sativus"
 /mol_type="mRNA"
 /strain="ronde rode kleine witpunt"
 /db_xref="taxon:3726"
 /tissue_type="seed"
 1..395
 /gene="Rs-APP1"
 15..257
 /gene="Rs-APP1"
 /function="antifungal, fungistatic"
 /codon_start=1
 /evidence=experimental
 /product="antifungal protein 1 preprotein"
 /protein_id="AA69541.1"
 /db_xref="GI:609322"
 /translation="MAKFAIIALLPAALVLFAPFAEAPTMTVEAQLCERPSGTWVGVC
 GNNAKNCQINLEAKRHGSCNYVFAHKCICVFPCC"
 15..101
 /gene="Rs-APP1"
 102..254
 /gene="Rs-APP1"
 /product="antifungal protein 1"
 /function="antifungal, fungistatic"
 /note="Evidence for antifungal activity: Analysis of two
 novel classes of antifungal proteins from radish (*Raphanus
 sativus* L.) seeds. Terras, F.R.G. et al. (1992), J. Biol.
 Chem. 267, 15301-15309"
 /citation=[1]
 /evidence=experimental
 395
 /gene="Rs-APP1"
 /note="18 A nucleotides"

polyA_signal
 Alignment Scores:
 Pred. No.: 2.07e-24 Length: 395
 Score: 283.00 Matches: 45
 Percent Similarity: 96.00% Conservative: 3
 Best Local Similarity: 90.00% Mismatches: 2
 Query Match: 92.79% Indels: 0
 DB: 8 Gaps: 0

US-10-681-972-2 (1-50) x RSU18557 (1-395)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
 Db 105 AAGTTGGCGGAAGGCCAAGTCGAGATGTCGAGAGTCTGTGGAACAAATACGCGATGC 164
 QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
 Db 165 AAGAATCAGTCATTAACCTTGAGAAAGCACACATGATCTTGCTTTCCCA 224
 QY 41 AlaHisLysCysIleCysTyrPheProCys 50
 Db 225 GCTCAAGTGCATCTGCTACTTTCCATGC 254

RESULT 10
 A26875
 LOCUS
 DEFINITION R.sativus APP1 gene.
 ACCESSION A26875
 VERSION A26875.1 GI:1247352
 KEYWORDS
 SOURCE Raphanus sativus (radish)
 ORGANISM Raphanus sativus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Rapphanus.

REFERENCE 1 (bases 1 to 414)

AUTHORS Broekaert, W.F., Cammue, B.P.A., Terras, F.R.G., Vanderleyden, J., Osborn, R.W. and Rees, S.B.

TITLE BIOCIDAL PROTEINS

JOURNAL Patent: WO 9305153-A 33 18-MAR-1993;

FEATURES

ICL PLC (GB)

Location/Qualifiers

1..414

/organism="Rapphanus sativus"

/mol_type="unassigned DNA"

/db_xref="taxon:3726"

ORIGIN

Alignment Scores:

Pred. No.: 2,18e-24 Length: 414

Score: 283.00 Matches: 45

Percent Similarity: 96.00% Conservative: 3

Best Local Similarity: 90.00% Mismatches: 2

Query Match: 92.79% Indels: 0

DB: 6 Gaps: 0

US-10-681-972-2 (1-50) x A26875 (1-414)

Qy 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20

Db 106 AAGTTGTGCGAAGGCCAAGTGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC 165

Qy 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40

Db 166 AAGAATCAGTGCATTAACTTGAAGAAGCAGCATGGATCTTGCAACTATGCTTCCCA 225

Qy 41 AlaHisLysCysIleCysTyrPheProCys 50

Db 226 GCTCACAAGTGTATCTGCTACTTTCCTTGT 255

RESULT 11

LOCUS A39549

DEFINITION Sequence 37 from Patent WO9416076.

ACCESSION A39549

VERSION A39549.1 GI:2295842

KEYWORDS

SOURCE unidentified

ORGANISM unclassified

REFERENCE 1 (bases 1 to 414)

AUTHORS Dubock, A.C., Powell, K.A. and Rees, S.B.

TITLE ANTIMICROBIAL-PROTEIN-PRODUCING ENDOSYMBIOTIC MICROORGANISMS

JOURNAL Patent: WO 9416076-A 37 21-JUL-1994;

ZENECA LTD (GB)

COMMENT Other publication AU 5820494 940815.

FEATURES

Location/Qualifiers

1..414

/organism="unidentified"

/mol_type="unassigned DNA"

/db_xref="taxon:32644"

ORIGIN

Alignment Scores:

Pred. No.: 2,18e-24 Length: 414

Score: 283.00 Matches: 45

Percent Similarity: 96.00% Conservative: 3

Best Local Similarity: 90.00% Mismatches: 2

Query Match: 92.79% Indels: 0

DB: 6 Gaps: 0

US-10-681-972-2 (1-50) x A39549 (1-414)

Qy 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20

Db 106 AAGTTGTGCGAAGGCCAAGTGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC 165

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Rapphanus.

REFERENCE 1 (bases 1 to 414)

AUTHORS Broekaert, W.F., Cammue, B.P.A., Terras, F.R.G., Vanderleyden, J., Osborn, R.W. and Rees, S.B.

TITLE BIOCIDAL PROTEINS

JOURNAL Patent: WO 9305153-A 33 18-MAR-1993;

FEATURES

ICL PLC (GB)

Location/Qualifiers

1..414

/organism="Rapphanus sativus"

/mol_type="unassigned DNA"

/db_xref="taxon:3726"

ORIGIN

Alignment Scores:

Pred. No.: 2,18e-24 Length: 414

Score: 283.00 Matches: 45

Percent Similarity: 96.00% Conservative: 3

Best Local Similarity: 90.00% Mismatches: 2

Query Match: 92.79% Indels: 0

DB: 6 Gaps: 0

US-10-681-972-2 (1-50) x A26875 (1-414)

Qy 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20

Db 106 AAGTTGTGCGAAGGCCAAGTGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC 165

Qy 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40

Db 166 AAGAATCAGTGCATTAACTTGAAGAAGCAGCATGGATCTTGCAACTATGCTTCCCA 225

Qy 41 AlaHisLysCysIleCysTyrPheProCys 50

Db 226 GCTCACAAGTGTATCTGCTACTTTCCTTGT 255

RESULT 12

LOCUS A63404

DEFINITION Sequence 19 from Patent WO9721814.

ACCESSION A63404

VERSION A63404.1 GI:3717176

KEYWORDS

SOURCE unidentified

ORGANISM unclassified

REFERENCE 1

AUTHORS Broekaert, W.F., De, S.G., Rees and Sarah, B.

TITLE ANTIFUNGAL PROTEINS

JOURNAL Patent: WO 9721814-A 19 19-JUN-1997;

ZENECA LTD (GB)

COMMENT Other publication AU 1105397 19970703.

FEATURES

Location/Qualifiers

1..414

/organism="unidentified"

/mol_type="unassigned DNA"

/db_xref="taxon:32644"

ORIGIN

Alignment Scores:

Pred. No.: 2,18e-24 Length: 414

Score: 283.00 Matches: 45

Percent Similarity: 96.00% Conservative: 3

Best Local Similarity: 90.00% Mismatches: 2

Query Match: 92.79% Indels: 0

DB: 6 Gaps: 0

US-10-681-972-2 (1-50) x A63404 (1-414)

Qy 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20

Db 106 AAGTTGTGCGAAGGCCAAGTGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC 165

Qy 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40

Db 166 AAGAATCAGTGCATTAACTTGAAGAAGCAGCATGGATCTTGCAACTATGCTTCCCA 225

Qy 41 AlaHisLysCysIleCysTyrPheProCys 50

Db 226 GCTCACAAGTGTATCTGCTACTTTCCTTGT 255

RESULT 13

LOCUS AR050153

DEFINITION Sequence 48 from patent US 5824869.

ACCESSION AR050153

VERSION AR050153.1 GI:5972145

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 414)

AUTHORS Broekaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B., Terras, F.R.G. and Vanderleyden, J.

TITLE BIOCIDAL PROTEINS

JOURNAL Patent: US 5824869-A 48 20-OCT-1998;

FEATURES

Location/Qualifiers

1..414

/organism="unknown"

/mol_type="unassigned DNA"

Qy 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40

Db 166 AAGAATCAGTGCATTAACTTGAAGAAGCAGCATGGATCTTGCAACTATGCTTCCCA 225

Qy 41 AlaHisLysCysIleCysTyrPheProCys 50

Db 226 GCTCACAAGTGTATCTGCTACTTTCCTTGT 255

RESULT 12

LOCUS A63404

DEFINITION Sequence 19 from Patent WO9721814.

ACCESSION A63404

VERSION A63404.1 GI:3717176

KEYWORDS

SOURCE unidentified

ORGANISM unclassified

REFERENCE 1

AUTHORS Broekaert, W.F., De, S.G., Rees and Sarah, B.

TITLE ANTIFUNGAL PROTEINS

JOURNAL Patent: WO 9721814-A 19 19-JUN-1997;

ZENECA LTD (GB)

COMMENT Other publication AU 1105397 19970703.

FEATURES

Location/Qualifiers

1..414

/organism="unidentified"

/mol_type="unassigned DNA"

/db_xref="taxon:32644"

ORIGIN

Alignment Scores:

Pred. No.: 2,18e-24 Length: 414

Score: 283.00 Matches: 45

Percent Similarity: 96.00% Conservative: 3

Best Local Similarity: 90.00% Mismatches: 2

Query Match: 92.79% Indels: 0

DB: 6 Gaps: 0

US-10-681-972-2 (1-50) x A63404 (1-414)

Qy 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20

Db 106 AAGTTGTGCGAAGGCCAAGTGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC 165

Qy 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40

Db 166 AAGAATCAGTGCATTAACTTGAAGAAGCAGCATGGATCTTGCAACTATGCTTCCCA 225

Qy 41 AlaHisLysCysIleCysTyrPheProCys 50

Db 226 GCTCACAAGTGTATCTGCTACTTTCCTTGT 255

RESULT 13

LOCUS AR050153

DEFINITION Sequence 48 from patent US 5824869.

ACCESSION AR050153

VERSION AR050153.1 GI:5972145

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 414)

AUTHORS Broekaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B., Terras, F.R.G. and Vanderleyden, J.

TITLE BIOCIDAL PROTEINS

JOURNAL Patent: US 5824869-A 48 20-OCT-1998;

FEATURES

Location/Qualifiers

1..414

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Alignment Scores: 2.18e-24 Length: 414
Pred. No.: 283.00 Matches: 45
Score: 283.00
Percent Similarity: 96.00% Conservative: 3
Best Local Similarity: 90.00% Mismatches: 2
Query Match: 92.79% Indels: 0
DB: 6 Gaps: 0

US-10-681-972-2 (1-50) x AR050153 (1-414)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 106 AAGTTGTGCGAAGGCCAAGTGGGACATGGTCAGAGTCTGTGGAAACAATAACGCATGC 165

QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 166 AAGATCAGTGCATTAACTTGGAGAACGACGACATGGATCTTGCAACTATGTCTTCCCA 225

QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 226 GCTCACAAGTGTATCTGCTACTTTCCTTGT 255

RESULT 14

LOCUS AR130272 414 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 48 from patent US 6187904.
ACCESSION AR130272
VERSION AR130272.1 GI:14118169

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 414)
AUTHORS Broekaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B.,
Terras, F.R.G. and Vanderleyden, J.
TITLE Biocidal proteins
JOURNAL Patent: US 6187904-A 48 13-FEB-2001;
FEATURES Location/Qualifiers
source 1..414
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores: 2.18e-24 Length: 414
Pred. No.: 283.00 Matches: 45
Score: 283.00
Percent Similarity: 96.00% Conservative: 3
Best Local Similarity: 90.00% Mismatches: 2
Query Match: 92.79% Indels: 0
DB: 6 Gaps: 0

US-10-681-972-2 (1-50) x AR130272 (1-414)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 106 AAGTTGTGCGAAGGCCAAGTGGGACATGGTCAGAGTCTGTGGAAACAATAACGCATGC 165

QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 166 AAGATCAGTGCATTAACTTGGAGAACGACGACATGGATCTTGCAACTATGTCTTCCCA 225

QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 226 GCTCACAAGTGTATCTGCTACTTTCCTTGT 255

RESULT 15

LOCUS I23728 414 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 48 from patent US 5538525.
ACCESSION I23728
VERSION I23728.1 GI:1603598

KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 414)
AUTHORS Broekaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B.,
Terras, F.R.G. and Vanderleyden, J.
TITLE Biocidal proteins
JOURNAL Patent: US 5538525-A 48 23-JUL-1996;
FEATURES Location/Qualifiers
source 1..414
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores: 2.18e-24 Length: 414
Pred. No.: 283.00 Matches: 45
Score: 283.00
Percent Similarity: 96.00% Conservative: 3
Best Local Similarity: 90.00% Mismatches: 2
Query Match: 92.79% Indels: 0
DB: 6 Gaps: 0

US-10-681-972-2 (1-50) x I23728 (1-414)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 106 AAGTTGTGCGAAGGCCAAGTGGGACATGGTCAGAGTCTGTGGAAACAATAACGCATGC 165

QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 166 AAGATCAGTGCATTAACTTGGAGAACGACGACATGGATCTTGCAACTATGTCTTCCCA 225

QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 226 GCTCACAAGTGTATCTGCTACTTTCCTTGT 255

Search completed: May 18, 2004, 21:15:13
Job time : 2173 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 18, 2004, 19:00:43 ; Search time 299 Seconds
(without alignments)
710.401 Million cell updates/sec

Title: US-10-681-972-2
Perfect score: 305
Sequence: 1 RLCRPSPTGWSGVCNNAC.....EHGSCNVFFPAHKICVFCFC 50

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 337383 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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9: Geneseqn2003cs: *
10: Geneseqn2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	305	100.0	270	2	Aat94582 Amplified
2	305	100.0	286	2	Aat94574 Alyssum s
3	305	100.0	481	2	Aat99289 Alyssum s
4	296	97.0	500	2	Aat94581 Composite
5	283	92.8	394	9	Adc51221 Brassica
6	283	92.8	414	2	Aaq38650 R8-APPI C
7	283	92.8	414	2	Aaq70128 Antimicro
8	283	92.8	414	2	Aat72333 Raphanus

9	283	92.8	414	2	Aat68696
10	283	92.8	426	9	Adc51223 Brassica
11	278	91.1	243	7	Ada68378 Arabidops
12	278	91.1	403	2	Aav10632 A. thalia
13	274	89.8	261	2	AAV10632
14	274	89.8	288	2	Aaq38652
15	274	89.8	244	3	AAQ70130
16	274	89.8	244	3	AAQ70130 Antimicro
17	274	89.8	524	3	AAZ53190 Raphanus
18	274	89.8	534	3	AAZ53196
19	274	89.8	534	3	AAZ53196 Portion o
20	274	89.8	534	3	AAZ53196 DNA encod
21	273	89.5	308	2	AAZ5326 DNA encod
22	265	86.9	243	6	ABZ14241 Cloned 5'
23	265	86.9	243	7	ABZ14241 Arabidops
24	265	86.9	243	7	ABZ14241 Arabidops
25	265	86.9	400	2	AAV10633 A. thalia
26	263	86.2	485	3	AAZ5337 DNA encod
27	259	84.9	434	3	AAZ5332 DNA encod
28	259	84.9	437	3	AAZ5331 DNA encod
29	259	84.9	443	3	AAZ5330 DNA encod
30	259	84.9	446	3	AAZ5329 DNA encod
31	259	84.9	485	3	AAZ5333 DNA encod
32	259	84.9	485	3	AAZ5335 DNA encod
33	259	84.9	488	3	AAZ5338 DNA encod
34	259	84.9	557	3	AAZ5336 DNA encod
35	259	84.9	575	3	AAZ5339 DNA encod
36	259	84.9	1093	3	AAZ5334 DNA encod
37	258	84.6	243	6	ABQ82690
38	258	84.6	414	3	AAZ39123
39	253	83.0	243	6	ABQ82691
40	253	83.0	416	3	AAZ39124
41	234	76.7	306	2	AAT94580
42	221	72.5	1973	3	AAZ46324
43	196	64.3	284	2	AAQ38651
44	196	64.3	284	2	AAQ70129
45	169	55.4	658	5	AAA54389

ALIGNMENTS

RESULT 1
AAT94582
ID AAT94582 standard; DNA; 270 BP.
XX
AC AAT94582;
XX
DT 12-MAY-1998 (first entry)
XX
DE Amplified Alyssum species antifungal polypeptide gene from pMON22652.
XX
KW Antifungal polypeptide; AlyAPP; inhibition; transgenic plant;
XX phytopathogenic fungus; resistance; ss.
XX
OS Alyssum sp.
XX
FH Key Location/Qualifiers
FT CDS 22..261
FT /tag= a
FT /product= "AlyAPP antifungal polypeptide"
FT sig_peptide 22..108
FT /tag= b
FT mat_peptide 109..258
FT /tag= c
XX

W09737024-A2.

us-10-681-972-2.p2n.rng

Wed May 19 11:30:05 2004

PA (MONS) MONSANTO CO.
 XX
 PI Liang J, Shah D, Wu Y, Rosenberger CA;
 XX
 DR WPI; 1997-503109/46.
 DR P-PSDB; AAW35560.
 XX
 PT Alyssum antifungal polypeptide and corresponding DNA - used in the
 PT production of transgenic plants resistant to phytopathogenic fungi.
 XX
 PS Example 4; Page 69; 92pp; English.
 XX
 CC This sequence represents the cDNA sequence cloned into the E. coli
 CC cassette vector pMON2317 to generate vector pMON22652. The cDNA encodes
 CC the antifungal polypeptide AlyAFP, isolated from plants of the genus
 CC Alyssum. The AlyAFP polypeptide can be used to control phytopathogenic
 CC fungi, whilst the coding DNA can be used to produce transgenic plants
 CC that express the polypeptide making them resistant to the phytopathogenic
 CC fungi

SQ Sequence 270 BP; 75 A; 58 C; 60 G; 75 T; 0 U; 2 Other;

Alignment Scores: 1.05e-26 Length: 270
 Pred. No.: 305.00 Matches: 50
 Score: 305.00 Conserv: 0
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Indels: 0
 Query Match: 100.00% Gaps: 0
 DB: 2

US-10-681-972-2 (1-50) x AAT94582 (1-270)

QY 1 ArgLeuGlyGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
 Db 109 AGTTGTGGAGAGACCAAGTGGCATGCTCAGGAGTTTGGGGAACAACATGCATGC 168
 QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
 Db 169 AGGAACCAATGCAGAACCTTGAAGAGCAGAACACGGATCTTGCACATATGCTTCCCA 228
 QY 41 AlaHisLysCysIleCysTyrPheProCys 50
 Db 229 GCTCACAATGATTTGTTACTTCCATGT 258

RESULT 2

AAT94574
 ID AAT94574 standard; cDNA; 286 BP.

XX AAT94574;

XX 12-MAY-1998 (first entry)

XX Alyssum species anti-fungal polypeptide AlyAFP cDNA sequence.

XX Antifungal polypeptide; AlyAFP; inhibition; transgenic plant;

XX phytopathogenic fungus; resistance; ss.

XX Alyssum sp.

XX Key Location/Qualifiers

XX 117..269

XX /tag= a

XX /product= "mature AlyAFP protein"

XX /note= "no start codon given at 5' end of sequence"

XX WO9737024-A2.

XX 09-OCT-1997.

XX 27-MAR-1997; 97WO-US005709.

XX 29-MAR-1996; 96US-00627706.

XX

PA (MONS) MONSANTO CO.
 XX
 PI Liang J, Shah D, Wu Y, Rosenberger CA;
 XX
 DR WPI; 1997-503109/46.
 DR P-PSDB; AAW35558.
 XX
 PT Alyssum antifungal polypeptide and corresponding DNA - used in the
 PT production of transgenic plants resistant to phytopathogenic fungi.
 XX
 PS Claim 12; Page 68; 92pp; English.

XX This sequence encodes the mature protein of an antifungal polypeptide
 CC (AlyAFP) isolated from plants of the genus Alyssum. The sequence was PCR
 CC amplified using primers AAT94583-T94584, and the resultant 264 bp
 CC fragment was cloned as a BamHI fragment into the expression vector
 CC pMON2317 to generate plasmid pMON22652. The AlyAFP sequence in this
 CC plasmid is placed under control of an E35S promoter and the maize HSP70
 CC intron 1 sequence. The protein can be used to control phytopathogenic
 CC fungi, whilst the DNA can be used to produce transgenic plants that
 CC express the protein making them resistant to the phytopathogenic fungi

SQ Sequence 286 BP; 80 A; 62 C; 65 G; 79 T; 0 U; 0 Other;

Alignment Scores: 1.13e-26 Length: 286
 Pred. No.: 305.00 Matches: 50
 Score: 305.00 Conserv: 0
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Indels: 0
 Query Match: 100.00% Gaps: 0
 DB: 2

US-10-681-972-2 (1-50) x AAT94574 (1-286)

QY 1 ArgLeuGlyGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
 Db 117 AGTTGTGGAGAGACCAAGTGGCATGCTCAGGAGTTTGGGGAACAACATGCATGC 176
 QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
 Db 177 AGGAACCAATGCAGAACCTTGAAGAGCAGAACACGGATCTTGCACATATGCTTCCCA 236
 QY 41 AlaHisLysCysIleCysTyrPheProCys 50
 Db 237 GCTCACAATGATTTGTTACTTCCATGT 266

RESULT 3

AAT99289

ID AAT99289 standard; DNA; 481 BP.

XX AAT99289;

XX 12-MAY-1998 (first entry)

XX Alyssum species AlyAFP cDNA sequence.

XX Antifungal polypeptide; AlyAFP; inhibition; transgenic plant;

XX phytopathogenic fungus; resistance; ss.

XX Alyssum sp.

XX Key Location/Qualifiers

XX 53..292

XX /tag= a

XX /product= "AlyAFP antifungal polypeptide"

XX sig_peptide

XX 53..139

XX /tag= b

XX mat_peptide

XX 140..289

XX /tag= c

XX polyA_signal

XX 439..443

XX /tag= d

XX WO9737024-A2.

XX

```

XX PD 09-OCT-1997.
XX PF 27-MAR-1997; 97WO-US005709.
XX PR 29-MAR-1996; 96US-00627706.
XX PA (MONS ) MONSANTO CO.
XX PI Liang J, Shah D, Wu Y, Rosenberger CA;
XX DR WPI; 1997-503109/46.
XX DR P-PSDB; AAW35560.
XX PT Alyssum antifungal polypeptide and corresponding DNA - used in the
XX PR production of transgenic plants resistant to phytopathogenic fungi.
XX PS Example 4; Fig 1; 92pp; English.
XX CC This sequence represents the cDNA sequence which encodes the antifungal
XX CC polypeptide AlyAPP, isolated from plants of the genus Alyssum. The AlyAPP
XX CC polypeptide can be used to control phytopathogenic fungi, whilst the
XX CC coding DNA can be used to produce transgenic plants that express the
XX CC polypeptide making them resistant to the phytopathogenic fungi
XX SQ Sequence 481 BP; 147 A; 88 C; 91 G; 154 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.: 2.14e-26 Length: 481
Score: 305.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-681-972-2 (1-50) x AAT94581 (1-481)
Qy 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 140 AGTTGTGCGAGAGACCAAGTGGACATGTCAGAGTTTGTGGGAACAACAATGCATGC 199
Qy 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 200 AGGAACCAATCGAAGAACCTTTGAAGAGCAGACACGATCTTGCACCTATGTCTTCCCA 259
Qy 41 AlahisLysCysIleCysTyrPheProCys 50
Db 260 GCTCACAATGTAATTGTACTTCCCATGT 289

RESULT 4
AAT94581
ID AAT94581 standard; DNA; 500 BP.
AC AAT94581;
XX 12-MAY-1998 (first entry)
DT 12-MAY-1998 (first entry)
DE Composite cDNA sequence for Alyssum species antifungal polypeptide.
KW Antifungal polypeptide; AlyAPP; inhibition; transgenic plant;
KW phytopathogenic fungus; resistance; ss.
XX Alyssum sp.
XX WO9737024-A2.
XX 09-OCT-1997.
XX 27-MAR-1997; 97WO-US005709.
XX 29-MAR-1996; 96US-00627706.
XX (MONS ) MONSANTO CO.

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XX LIANG J, Shah D, Wu Y, Rosenberger CA;
XX WPI; 1997-503109/46.
XX Alyssum antifungal polypeptide and corresponding DNA - used in the
XX production of transgenic plants resistant to phytopathogenic fungi.
XX Example 4; Page 67; 92pp; English.
XX This sequence represents the cDNA sequence encoding the antifungal
XX polypeptide AlyAPP, from plants of the genus Alyssum. The sequence
XX represents a composite of the sequences isolated by 5' and 3' RACE (Rapid
XX Amplification of cDNA Ends) methods (see AAT94577 and AAT94580). The
XX AlyAPP polypeptide can be used to control phytopathogenic fungi, whilst
XX the coding DNA can be used to produce transgenic plants that express the
XX polypeptide making them resistant to the phytopathogenic fungi
XX SQ Sequence 500 BP; 145 A; 89 C; 111 G; 154 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.: 2.5e-25 Length: 500
Score: 296.00 Matches: 48
Percent Similarity: 98.00% Conservative: 1
Best Local Similarity: 96.00% Mismatches: 1
Query Match: 97.05% Indels: 0
DB: 2 Gaps: 0

US-10-681-972-2 (1-50) x AAT94581 (1-500)
Qy 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 159 AAGTTGTGCGAGAGTCCCAAGTGGACATGTCAGAGTTTGTGGGAATAATAACGCATGC 218
Qy 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 219 AGGAACCAATCGAAGAACCTTTGAAGAGCAGACACGATCTTGCACCTATGTCTTCCCA 278
Qy 41 AlahisLysCysIleCysTyrPheProCys 50
Db 279 GCTCACAATGTAATTGTACTTCCCATGT 308

RESULT 5
ADC51221
ID ADC51221 standard; DNA; 394 BP.
AC ADC51221;
XX 18-DEC-2003 (first entry)
DT 18-DEC-2003 (first entry)
DE Brassica oleracea defensin protein coding sequence.
KW antimicrobial protein; defensin; transgenic plant;
KW composite disease resistance; pathogenic bacteria;
KW rice white leaf blight; brown-stripe disease; glume blight;
KW seedling damping-off disease; filamentous fungi; rice blight;
KW sheath blight disease; leaf blight; gene; ds.
XX Brassica oleracea.
XX Key Location/Qualifiers
XX CDS 1..243
XX /tag= a
XX /product= "Brassica oleracea defensin protein"
XX JP2003088379-A.
XX 25-MAR-2003.
XX 18-SEP-2001; 2001JP-00283117.
XX 18-SEP-2001; 2001JP-00283117.
XX

```

us-10-681-972-2.2.p2n.rng

Wed May 19 11:30:05 2004

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PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
XX
XX WPI: 2003-621123/59.
DR P-FSDB; ADC51222.
XX
XX Novel protein from Brassica campestris, useful as antimicrobial against
PT plant pathogenic filamentous fungi or pathogenic bacteria, especially for
PT treating e.g. rice white leaf blight and sheath blight disease.
XX
XX Claim 3; SEQ ID NO 1; 34pp; Japanese.
XX
XX The invention comprises the amino acid and coding sequences of
CC antimicrobial (defensin) proteins from Brassica. The DNA and protein
CC sequences of the invention are useful for producing transformed plants
CC with composite disease resistance, especially resistant to diseases
CC caused by pathogenic bacteria, such as: rice white leaf blight, brown-
CC stripe disease, glume blight, and seedling damping-off disease. As well
CC as diseases caused by filamentous fungi, such as: rice blight, sheath
CC blight disease, and leaf blight. The present DNA sequence encodes a
CC Brassica defensin protein of the invention.
XX
XX Sequence 394 BP; 116 A; 71 C; 82 G; 125 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 6.08e-24 Length: 394
Score: 283.00 Matches: 45
Percent Similarity: 96.00% Conservatives: 3
Best Local Similarity: 90.00% Mismatches: 2
Query Match: 92.79% Indels: 0
DB: 9 Gaps: 0
US-10-681-972-2 (1-50) x ADC51221 (1-394)
QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 91 AAGTTGCGAGAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAACAATAACGCATGC 150
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 151 AAGAATCAGTCATTAACTTGAGAAAGCAGCAGCATGTCCTTGCACATGCTCTTCCCA 210
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 211 GCTCAAGTGTATTGCTACTTCTTCTTCTTCT 240
RESULT 6
AAQ38650
ID AAQ38650 standard; DNA; 414 BP.
XX
XX AAQ38650;
AC
XX
XX 25-MAR-2003 (revised)
DT 07-JUL-1993 (first entry)
XX
XX Rs-APPI cDNA.
DE
XX Raphanus sativus; Brassica; Arabidopsis; Chicus; Lathyrus; Clitoria;
KW fungicide; bactericide; antibiotic; antifungal; gram positive;
KW plant disease resistance; low toxicity.
XX
XX Raphanus sativus.
OS
XX Key Location/Qualifiers
FH 16..256
FT CDS /*tag= a
FT
XX
XX WO9305153-A1.
FN
XX
XX 18-MAR-1993.
PD
XX
XX 27-AUG-1992; 92WO-GB001570.
PF
XX
XX 29-AUG-1991; 91GB-00018523.
PR

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PR 13-FEB-1992; 92GB-00003038.
PR 25-JUN-1992; 92GB-00013526.
XX
XX (ICIL) IMPERIAL CHEM IND PLC.
PA
XX Broekaert WF, Cammue BPA, Osborn RW, Rees SB, Terras FRG;
PI Vanderleyden J;
XX
XX WPI; 1993-100978/12.
XX
XX Biocidal proteins isolated from seeds of plants - e.g. brassica or
FT dahlia, useful for increasing plants' resistance to fungal and bacterial
FT diseases.
XX
XX Example 21; Fig 35; 110pp; English.
XX
XX This cDNA represents the sequence of Rs-APPI from Raphanus sativus. PCR
CC primer AAQ38640 was used together with AAQ38641 to generate a probe for
CC screening a Raphanus sativus seed cDNA library. This primer corresponds
CC to amino acids 2 to 7 of Rs-APPI and has a sense orientation. The 144bp
CC product was partially re-amplified using AAQ38642 and AAQ38641 to give a
CC 123bp product, which was further reamplified with the same primers and
CC digoxigenin-11-dump instead of dTTP to give a digoxigenin labeled PCR
CC product. This was used to screen a lambda ZAPII cDNA library by in situ
CC plaque hybridisation. Positive plaques were purified and subjected to
CC additional screening rounds with the same probe. Inserts were excised in
CC vivo into the pBluescript phagemid form with the aid of helper phage
CC R408. Inserts from 22 positive clones were excised by EcoRI digestion and
CC their size compared by agarose gel electrophoresis. Four clones had
CC insert sizes of approx. 400bp the others between 250-300bp. The inserts
CC of the 4 largest clones were then sequenced and found to differ only in
CC the length of their 5' and 3' UTR's. The longest sequence is given here.
CC (Updated on 25-MAR-2003 to correct FN field.)
XX
XX SQ Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 6.46e-24 Length: 414
Score: 283.00 Matches: 45
Percent Similarity: 96.00% Conservatives: 3
Best Local Similarity: 90.00% Mismatches: 2
Query Match: 92.79% Indels: 0
DB: 2 Gaps: 0
US-10-681-972-2 (1-50) x AAQ38650 (1-414)
QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 106 AAGTTGCGAGAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAACAATAACGCATGC 165
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 166 AAGAATCAGTCATTAACTTGAGAAAGCAGCAGCATGTCCTTGCACATGCTCTTCCCA 225
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 226 GCTCAAGTGTATTGCTACTTCTTCTTCTTCT 255
RESULT 7
AAQ70128
ID AAQ70128 standard; cDNA; 414 BP.
XX
XX AAQ70128;
AC
XX
XX 25-MAR-2003 (revised)
DT 14-FEB-1995 (first entry)
XX
XX Antimicrobial Rs-APPI.
DE
XX Antimicrobial; Rs-APPI; symbiosis; disease-resistance; fungus-resistance;
KW Clavibacter xyli subsp. cynodontis; Cxc; crop improvement; endophyte; ss.
XX
XX Raphanus sativus.
OS

```


XX WO9416076-A1.
XX 21-JUL-1994.
XX 05-JAN-1994; 94WO-GB0000012.
XX 08-JAN-1993; 93GB-00000281.
XX (ZENE) ZENECA LTD.
XX Dubock AC, Powell KA, Rees SB;
XX WPI; 1994-249223/30.
XX P-PSDB; AAR57325.
XX Antimicrobial protein producing endo-symbiotic microorganisms - is
XX produced by combining nucleic acids encoding the protein with an
XX endophyte, useful for protecting plant hosts from esp. fungal disease.
XX Disclosure; Page 31; 39pp; English.
XX Plant-derived antimicrobial proteins are expressed in endosymbiotic
XX Clavibacter xyli subsp. cynodontis (Cxc). Plants or seeds treated with
XX recombinant Cxc are protected against fungal disease. A suitable
XX antimicrobial protein is Rs-AFP1 from R. sativus. The full-length cDNA
XX sequence of Rs-AFP1 is given in AAQ70128. (Updated on 25-MAR-2003 to
XX correct PN field.)
XX Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
Alignment Scores: Length: 414
Pred. No.: 283.00 Matches: 45
Score: 283.00
Percent Similarity: 96.00% Conservative: 3
Best Local Similarity: 90.00% Mismatches: 2
Query Match: 92.79% Indels: 0
DB: 2 Gaps: 0
US-10-681-972-2 (1-50) x AAQ70128 (1-414)
QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 106 AAGTTGTGCGAAGGCCAAGTGGACATGTCAGGAGTCTGTGGAACAATAACGCATGC 165
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 166 AAGAATCAGTGCATTAACCTTGAGAAAGCAGCAGCATGGATCTTGCAACTATGCTTCCCA 225
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 226 GCTCACAGGTATCTGCTACTTCTTGT 255
RESULT 8
AAT72333
ID AAT72333 standard; cDNA; 414 BP.
XX AAT72333;
XX 25-MAR-2003 (revised)
XX 19-JAN-1998 (first entry)
XX Raphanus sativus antifungal protein I (Rs-AFP1) cDNA.
XX Antifungal protein; candida; fungal resistance; food additive; radish;
XX crop protection; plant defensin; bacterial protection; preservative; ss.
XX Raphanus sativus.
XX Key Location/Qualifiers
XX CDS 16..258
XX /*tag= a
XX /transl_except= (pos:85..87, aa:Glu)

FT sig_peptide 16..102
FT /*tag= b
FT mat_peptide 103..255
FT /*tag= c
FT /product= "antifungal_protein_1"
XX WO9721815-A2.
XX 19-JUN-1997.
XX 12-DEC-1996; 96WO-GB003068.
XX 13-DEC-1995; 95GB-00025455.
XX 28-MAR-1996; 96GB-00006552.
XX (ZENE) ZENECA LTD.
XX Melloen RH, Puijk WC, Schaaper WMM, Sijtsma L, Van Amerongen A;
XX Broekaert W, Samblanx GW, Fant F, Borremans FAM, Rees SB;
XX Van Gelder WMJ;
XX WPI; 1997-332786/30.
XX P-PSDB; AAW19280.
XX Antifungal peptide derived from radish antifungal protein 2 - and related
XX DNA, useful for producing plants with increased fungal resistance and as
XX therapeutic or preservative agent.
XX Claim 8; Fig 2; 65pp; English.
XX This cDNA sequence encodes an Rhamnus sativus (radish) antifungal
XX protein (Rs-AFP1). Analogues of the homologous protein, Rs-AFP2
XX (AAW19281), have also been produced [see AAW19282-92, AAW19294-98,
XX AAW19301-04, AAW19330-34 and AAW1965-834]. Plants containing DNA
XX sequences encoding these proteins have improved resistance to fungi.
XX Compositions containing the peptides can be used to control fungi or
XX bacteria in pharmaceutical (e.g. treatment of Candida infections) or
XX preservative purposes (as food additives). In agriculture, the peptide
XX may be used to improve disease resistance or disease tolerance of crops,
XX either pre or post harvest. When applied to plants they may also have
XX curative as well as protective actions. The peptides may also be used to
XX protect plants by introducing them, or a microorganism capable of
XX expressing the peptide into the soil. (Updated on 25-MAR-2003 to correct
XX Pf field.)
XX Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
Alignment Scores: Length: 414
Pred. No.: 6.46e-24 Matches: 45
Score: 283.00
Percent Similarity: 96.00% Conservative: 3
Best Local Similarity: 90.00% Mismatches: 2
Query Match: 92.79% Indels: 0
DB: 2 Gaps: 0
US-10-681-972-2 (1-50) x AAT72333 (1-414)
QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 106 AAGTTGTGCGAAGGCCAAGTGGACATGTCAGGAGTCTGTGGAACAATAACGCATGC 165
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 166 AAGAATCAGTGCATTAACCTTGAGAAAGCAGCAGCATGGATCTTGCAACTATGCTTCCCA 225
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 226 GCTCACAGGTATCTGCTACTTCTTGT 255
RESULT 9
AAT68696
ID AAT68696 standard; cDNA; 414 BP.
XX

[illegible]

Db 211 GCTCACAAGTGATTTGCTACTTCCCTTGT 240

RESULT 11

ADA68378

ID ADA68378 standard; DNA; 243 BP.

XX AC ADA68378;

XX DT 20-NOV-2003 (first entry)

XX DE Arabidopsis thaliana gene, SEQ ID 747.

XX KW Plant; bacterial infection; fungal infection; viral infection; ds.

XX OS Arabidopsis thaliana.

XX PN W02003000898-A1.

XX PD 03-JAN-2003.

XX PF 22-JUN-2001; 2001WO-IB001105.

XX PR 22-JUN-2001; 2001WO-IB001105.

XX PA (SYGN) SYNGENTA PARTICIPATIONS AG.

XX PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;

XX PI Katagiri F, Qian S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;

XX DR WPI; 2003-175290/17.

XX PT Identifying at least one gene involved in plant resistance or response to

XX PT pathogenic infection for conferring resistance or tolerance to a plant to

XX PT bacterial, fungal or viral infection by determining or detecting plant

XX PT gene expression.

XX PS Claim 6; SEQ ID NO 747; 899pp; English.

XX CC The present invention relates to a method (M1) for identifying genes

XX CC involved in plant resistance or response to pathogenic infection. M1

XX CC comprises identifying a gene whose expression is significantly altered in

XX CC the incompatible interaction of plant gene expression relative to

XX CC expression of the gene in an uninfected plant, in a mutant plant that

XX CC does not express a gene associated with response to pathogenic infection,

XX CC or in a corresponding incompatible or compatible interaction. (M1) is

XX CC useful for conferring resistance to resistance or tolerance to a plant to

XX CC bacterial, fungal or viral infection. The present sequence was used to

XX CC illustrate the invention.

XX SQ Sequence 243 BP; 58 A; 56 C; 59 G; 70 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.28e-23 Length: 243

Score: 278.00 Matches: 44

Percent Similarity: 96.00% Conservative: 4

Best Local Similarity: 88.00% Mismatches: 2

Query Match: 91.15% Indels: 0

DB: 7 Gaps: 0

US-10-681-972-2 (1-50) x ADA68378 (1-243)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20

Db 91 AAGTTGTGGAGAGGCAAGTGGGACATGGTCCGGAGTTTGGGAAACAGTAACGGTGC 150

QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40

Db 151 AAGAATCAGTGCAATTAACTTGGAAAGCAGCAGCATGGATCTTGCAACTATGCTTCCCA 210

QY 41 AlaHisLysCysIleCysTyrPheProCys 50

Db 211 GCTCACAATGATATCTGCTACTTCCCATGT 240

RESULT 12

AAV10632

ID AAV10632 standard; DNA; 403 BP.

XX AC AAV10632;

XX DT 23-JUN-1998 (first entry)

XX DE A. thaliana PDF1.1 DNA.

XX KW Defensin; PDF1.1; protection; plant; pathogen; jasmonate; ethylene;

XX KW fungi; ss.

XX OS Arabidopsis thaliana.

XX FH Key Location/Qualifiers

FT CDS 26..268

FT sig_peptide /tag= a

FT mat_peptide /tag= b

FT /tag= c

FT /product= "PDF1.1"

FT /note= "plant defensin"

XX PN W09800023-A2.

XX PD 08-JAN-1998.

XX PF 20-JUN-1997; 97WO-GB001672.

XX PR 01-JUL-1996; 96GB-00013753.

XX PA (ZENE) ZENECA LTD.

XX PI Broekaert WF, Thomma BPHJ, Penninckx IAMA, Terras PRG, Manners JM;

XX PI Kazan K;

XX WPI; 1998-086663/08.

XX P-PSDB; AAW40345.

XX PT Protecting plants against pathogens by inducing defensin genes - by

XX PT stimulating ethylene or jasmonate pathways, also new promoter of defensin

XX PT gene from Arabidopsis.

XX PS Disclosure; Fig 1; 72pp; English.

XX CC This sequence encodes the Arabidopsis PDF1.1 gene which is used in a

XX CC novel method for the protection of plants against pathogens which

XX CC involves inducing expression of a plant defensin gene by stimulating the

XX CC jasmonate and/or ethylene pathways. The method is used to induce

XX CC protection against necrotrophic pathogens, specifically fungi and does

XX CC not require cytotoxic or potentially harmful chemicals

XX SQ Sequence 403 BP; 112 A; 77 C; 85 G; 129 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2.39e-23 Length: 403

Score: 278.00 Matches: 44

Percent Similarity: 96.00% Conservative: 4

Best Local Similarity: 88.00% Mismatches: 2

Query Match: 91.15% Indels: 0

DB: 2 Gaps: 0

US-10-681-972-2 (1-50) x AAV10632 (1-403)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20

Db 116 AAGTTGTGGAGAGGCAAGTGGGACATGGTCCGGAGTTTGGGAAACAGTAACGGTGC 175

QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40

Db 176 AAGAATCAGTGCAATTAACTTGGAAAGCAGCAGCATGGATCTTGCAACTATGCTTCCCA 235

QY 41 AlaHisLysCysLeuPheProCys 50
 DB 236 GCTCACAATGATCTGCTACTTCCCATGT 265

RESULT 13
 AAQ38652 ID AAQ38652 standard; DNA; 261 BP.
 AC AAQ38652;
 XX 25-MAR-2003 (revised)
 DT 07-JUL-1993 (first entry)
 XX Rs-AFP2 cDNA.
 XX Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria;
 KW fungicide; bacteriocide; antibiotic; antifungal; gram positive;
 KW plant disease resistance; low toxicity.
 XX Raphanus sativus.
 XX
 XX Key Location/Qualifiers
 FH 16..256
 FT CDS /*tag= a
 FT
 XX WO9305153-A1.
 XX 18-MAR-1993.
 XX 27-AUG-1992; 92WO-GB001570.
 XX 29-AUG-1991; 91GB-00018523.
 PR 13-FEB-1992; 92GB-00003038.
 PR 25-JUN-1992; 92GB-00013526.
 XX (ICIL) IMPERIAL CHEM IND PLC.
 XX Broekaert WF, Cammue BPA, Osborn RW, Rees SB, Terras PRG;
 PI Vanderleyden J;
 XX WPI; 1993-100978/12.
 DR Biocidal proteins isolated from seeds of plants - e.g. brassica or
 PT dahlia, useful for increasing plants' resistance to fungal and bacterial
 PT diseases.
 XX Example 21; Fig 35; 110pp; English.
 XX This cDNA represents the sequence of Rs-AFP2 from Raphanus sativus. PCR
 CC primer AAQ38640 was used together with AAQ38641 to generate a probe for
 CC screening a Raphanus sativus seed cDNA library. This primer corresponds
 CC to amino acids 2 to 7 of Rs-AFP1 and has a sense orientation. The 144bp
 CC product was partially re-amplified using AAQ38642 and AAQ38641 to give a
 CC 123bp product, which was further reamplified with the same primers and
 CC digoxigenin-11-dUTP instead of dTTP to give a digoxigenin labeled PCR
 CC product. This was used to screen a lambda ZAPII cDNA library by in situ
 CC plaque hybridisation. Positive plaques were purified and subjected to two
 CC additional screening rounds with the same probe. Inserts were excised in
 CC vivo into the pBluescript phagemid form with the aid of helper phage
 CC R408. Inserts from 22 positive clones were excised by EcoRI digestion and
 CC their size compared by agarose gel electrophoresis. Four clones had
 CC insert sizes of approx. 400bp the others between 250-300bp. The inserts
 CC of the 4 largest clones were then sequenced and found to differ only in
 CC the length of their 5' and 3' UTR's. The longest sequence was identified
 CC as Rs-AFP1 (AAQ38650). Rs-AFP2 was seen to differ by only 2 amino acids
 CC from Rs-AFP1, so the Rs-AFP1 cDNA was transformed to the Rs-AFP2
 CC nucleotide sequence by PCR assisted site directed mutagenesis. (Updated
 CC on 25-MAR-2003 to correct FN field.)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
 DB 106 AAGTTGTGCCAAAGGCCCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACCATGC 165

QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
 DB 166 AAGATCATGTCATTAGACTTGGAGAACACGACATGGATCTTGCACATATGCTCTTCCCA 225

QY 41 AlaHisLysCysLeuPheProCys 50
 DB 236 GCTCACAATGATCTGCTACTTCCCATGT 255

RESULT 14
 AAQ70130 ID AAQ70130 standard; cDNA; 288 BP.
 XX AAQ70130;
 XX 25-MAR-2003 (revised)
 DT 14-FEB-1995 (first entry)
 XX Antimicrobial Rs-AFP2.
 XX Antimicrobial; Rs-AFP2; symbiosis; disease-resistance; fungus-resistance;
 KW Clavibacter xyli subsp. cynodontis; Cxc; crop improvement; endophyte;
 KW PCR; polymerase chain reaction; mutagenesis; ss.
 XX Raphanus sativus.
 XX WO9416076-A1.
 XX 21-JUL-1994.
 XX 05-JAN-1994; 94WO-GB000012.
 XX 08-JAN-1993; 93GB-00000281.
 XX (ZENE) ZENECA LTD.
 XX Dubock AC, Powell KA, Rees SB;
 XX WPI; 1994-249223/30.
 XX P-PSDB; AAR57327.
 XX Antimicrobial protein producing endo-symbiotic microorganisms - is
 PT produced by combining nucleic acids encoding the protein with an
 PT endophyte, useful for protecting plant hosts from esp. fungal disease.
 XX Disclosure; Page 33; 39pp; English.
 XX Plant-derived antimicrobial proteins are expressed in endosymbiotic
 CC Clavibacter xyli subsp. cynodontis (Cxc). Plants or seeds treated with
 CC recombinant Cxc are protected against fungal disease. A suitable
 CC antimicrobial protein is Rs-AFP1 from R. sativus. The full-length cDNA
 CC sequence of PCR assisted site-directed mutagenesis of Rs-AFP2 is given in
 CC AAQ70130 and the deduced amino acid sequence in AAR57327. (Updated on 25-
 CC MAR-2003 to correct FN field.)

QY Sequence 288 BP; 70 A; 66 C; 69 G; 83 T; 0 U; 0 Other;
 XX Alignment Scores:
 XX Pred. No.: 4.61e-23 Length: 288
 XX Score: 274.00 Matches: 43
 XX Percent Similarity: 94.00% Conservative: 4

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model
Run on: May 18, 2004, 20:26:28 ; Search time 63 Seconds
(without alignments)
440.437 Million cell updates/sec

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Searched: 682709 seqs, 277475446 residues

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	305	100.0	270	1	US-08-627-706-14
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4	305	100.0	286	1	US-08-627-706-12
5	305	100.0	286	3	US-09-103-489-12
6	305	100.0	286	4	US-09-829-381D-12
7	296	97.0	500	1	US-08-627-706-9
8	296	97.0	500	3	US-09-103-489-9
9	296	97.0	500	4	US-09-829-381D-9
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23	274	89.8	288	3	US-08-971-982-58
24	273	89.5	308	1	US-08-627-706-5
25	273	89.5	308	3	US-09-103-489-5
26	273	89.5	308	4	US-09-829-381D-5
27	234	76.7	306	1	US-08-627-706-8
28	234	76.7	306	3	US-09-103-489-8
29	234	76.7	306	4	US-09-829-381D-8
30	196	64.3	284	1	US-08-377-687-50
31	196	64.3	284	1	US-08-777-192-50
32	196	64.3	284	3	US-08-971-982-50
33	157	51.5	150	1	US-08-377-687-31
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37	154	50.5	150	1	US-08-777-192-34
38	154	50.5	150	3	US-08-971-982-34
39	152	49.8	150	1	US-08-377-687-33
40	152	49.8	150	1	US-08-777-192-33
41	152	49.8	150	3	US-08-971-982-33
42	151.5	49.7	147	1	US-08-377-687-36
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44	151.5	49.7	147	3	US-08-971-982-36
45	149	48.9	565	4	US-09-589-733C-6

ALIGNMENTS

RESULT 1

US-08-627-706-14
; Sequence 14, Application US/08627706
; Patent No. 5773696
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. 5773696th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/627,706
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21(10700)A
; TELEPHONE: (314)537-6224
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:
LENGTH: 270 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-627-706-14

Alignment Scores:
Pred. No.: 9.41e-31 Length: 270
Score: 305.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-681-972-2 (1-50) x US-08-627-706-14 (1-270)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
DB 109 AGGTTGTGGAGAGACCAAGTGGGACATGTTGAGGAGTTTGTGGGACCAACATGCGATGC 168
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
DB 169 AGGAACCAATGCAGAAACCTTGAAGAGCAGACACGGATCTTGCACATATGTCTTCCCA 228
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
DB 229 GCTCACAATGTATTGTTACTTCCCATGT 258

RESULT 2

US-09-103-489-14
; Sequence 14, Application US/09103489
; Patent No. 6215048
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yennie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. 6215048th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,489
FILING DATE: 24-JUN-1998
CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-6224
TELEFAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 270 base pairs
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-103-489-14

Alignment Scores:

Pred. No.: 9.41e-31 Length: 270
Score: 305.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-681-972-2 (1-50) x US-09-103-489-14 (1-270)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
DB 109 AGGTTGTGGAGAGACCAAGTGGGACATGTTGAGGAGTTTGTGGGACCAACATGCGATGC 168
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
DB 169 AGGAACCAATGCAGAAACCTTGAAGAGCAGACACGGATCTTGCACATATGTCTTCCCA 228
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
DB 229 GCTCACAATGTATTGTTACTTCCCATGT 258

RESULT 3

US-09-829-381D-14
; Sequence 14, Application US/09829381D
; Patent No. 6653280
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yennie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alyssum and Methods for Control
; TITLE OF INVENTION: Plant Pathogenic Fungi
; FILE REFERENCE: 38-21 (10700) C
; CURRENT APPLICATION NUMBER: US/09/829,381D
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/103,489
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 270
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid
US-09-829-381D-14

Alignment Scores:

Pred. No.: 9.41e-31 Length: 270
Score: 305.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-681-972-2 (1-50) x US-09-829-381D-14 (1-270)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
DB 109 AGGTTGTGGAGAGACCAAGTGGGACATGTTGAGGAGTTTGTGGGACCAACATGCGATGC 168
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
DB 169 AGGAACCAATGCAGAAACCTTGAAGAGCAGACACGGATCTTGCACATATGTCTTCCCA 228
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
DB 229 GCTCACAATGTATTGTTACTTCCCATGT 258

RESULT 4

US-08-627-706-12

; Sequence 12, Application US/08627706
; Patent No. 5773696
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yennie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. 5773696th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08627,706
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21(10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6224
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-627-706-12

Alignment Scores:
Pred. No.: 1,02e-30 Length: 286
Score: 305.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-681-972-2 (1-50) x US-08-627-706-12 (1-286)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 117 AGGTTGTGGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACATGCATGC 176

QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 177 AGGAACCAATGCAGAAACCTTGAAGAGACAGACGATCTTGCACATATGCTTCCCA 236

QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 237 GCTCACAATGTATTGTACTTCCCATGT 266

RESULT 5
US-09-103-489-12
; Sequence 12, Application US/09103489
; Patent No. 6215048
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yennie S.
; APPLICANT: Rosenberger, Cindy A.

; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. 6215048th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09103,489
; FILING DATE: 24-JUN-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21 (10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 537-6224
; TELEFAX: (314) 537-6047
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-103-489-12

Alignment Scores:
Pred. No.: 1.02e-30 Length: 286
Score: 305.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-681-972-2 (1-50) x US-09-103-489-12 (1-286)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 117 AGGTTGTGGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACATGCATGC 176

QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 177 AGGAACCAATGCAGAAACCTTGAAGAGACAGACGATCTTGCACATATGCTTCCCA 236

QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 237 GCTCACAATGTATTGTACTTCCCATGT 266

RESULT 6
US-09-829-381D-12
; Sequence 12, Application US/09829381D
; Patent No. 6653280
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yennie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide ALVAFP from Alyssum and Methods for Control
; Controlling Plant Pathogenic Fungi
; FILE REFERENCE: 38-21 (10700) C
; CURRENT APPLICATION NUMBER: US/09/829,381D
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/103,489
; PRIOR FILING DATE: 1998-06-24

1 NUMBER OF SEQ ID NOS: 20
2 SOFTWARE: PatentIn version 3.1
3 SEQ ID NO 12
4 LENGTH: 286
5 TYPE: DNA
6 ORGANISM: Artificial Sequence
7 FEATURE:
8 OTHER INFORMATION: Synthetic PCR reaction product
9 US-09-829-381D-12

Alignment Scores:
Pred. No.: 1,02e-30 Length: 286
Score: 305.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Indels: 0
Query Match: 100.00%
DB: 4 Gaps: 0

US-10-681-972-2 (1-50) x US-09-829-381D-12 (1-286)

QY 1 ArgLeuCyGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 117 AGTTGTGGAGAGACCAAGTGGACATGTCAGGAGTTTGTGGGAACACATGTCATGC 176
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 177 AGGAACCAATGCAGAACCTTGAAGAGAGACGATCTTGCACACTATGCTTCCCA 236
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 237 GCTCACAATGTTTGTACTTCCCATGT 266

RESULT 7

US-08-627-706-9
Sequence 9, Application US/08627706
Patent No. 5773696
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yannie S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
CONTROLLING PLANT PATHOGENIC FUNGI
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 5773696th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,706
FILING DATE:
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21(10700)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6224
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

1 MOLECULE TYPE: cDNA
2 US-08-627-706-9

Alignment Scores:
Pred. No.: 3,05e-29 Length: 500
Score: 296.00 Matches: 48
Percent Similarity: 98.00% Conservative: 1
Best Local Similarity: 96.00% Mismatches: 1
Indels: 0
Query Match: 97.05%
DB: 1 Gaps: 0

US-10-681-972-2 (1-50) x US-08-627-706-9 (1-500)

QY 1 ArgLeuCyGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 159 AAGTTGTGGAGAGTCCCAAGTGGACATGTCAGGAGTTTGTGGGAATAATAACGCATGC 218
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 219 AGGAACCAATGCAGAACCTTGAAGAGAGACGATCTTGCACACTATGCTTCCCA 278
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 279 GCTCACAATGTTTGTACTTCCCATGT 308

RESULT 8

US-09-103-489-9
Sequence 9, Application US/09103489
Patent No. 6215048
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yannie S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
CONTROLLING PLANT PATHOGENIC FUNGI
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 6215048th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,489
FILING DATE: 24-JUN-1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-6224
TELEFAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 500 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-103-489-9
Alignment Scores:
Pred. No.: 3,05e-29 Length: 500
Score: 296.00 Matches: 48
Percent Similarity: 98.00% Conservative: 1

APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi

NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 6215048th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/103,489
FILING DATE: 24-JUN-1998
CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-6224
TELEFAX: (314) 537-6047

INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:

LENGTH: 285 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
US-09-103-489-16

Alignment Scores:
Pred. No.: 6.7e-28 Length: 285
Score: 283.00 Matches: 45
Percent Similarity: 96.00% Conservative: 3
Best Local Similarity: 90.00% Mismatches: 2
Query Match: 92.79% Indels: 0
DB: 3 Gaps: 0

US-10-681-972-2 (1-50) x US-09-103-489-16 (1-285)

Qy 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 121 AAGTTGTGCGAGAGCCATCAGGGACTTGGTCAGGAGTCTGGGAAACAACACCGCATGC 180
Qy 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 181 AAGAACCACATGCATCAACCTCGAGAAGCGACGCGCATGGATCTTGCAACTACGCTCTCCCA 240
Qy 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 241 GCTCAAGTGCATCTGCTACTTTCCATGC 270

RESULT 12

US-09-829-381D-16
Sequence 16, Application US/09829381D
Patent No. 6653280
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide ALXAPP from Alyseum and Methods for Control
FILE REFERENCE: 38-21 (10700) C
CURRENT APPLICATION NUMBER: US/09/829,381D
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/103,489
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20

SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 285
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-829-381D-16

Alignment Scores:
Pred. No.: 6.7e-28 Length: 285
Score: 283.00 Matches: 45
Percent Similarity: 96.00% Conservative: 3
Best Local Similarity: 90.00% Mismatches: 2
Query Match: 92.79% Indels: 0
DB: 4 Gaps: 0

US-10-681-972-2 (1-50) x US-09-829-381D-16 (1-285)

Qy 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 121 AAGTTGTGCGAGAGCCATCAGGGACTTGGTCAGGAGTCTGGGAAACAACACCGCATGC 180
Qy 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 181 AAGAACCACATGCATCAACCTCGAGAAGCGACGCGCATGGATCTTGCAACTACGCTCTCCCA 240
Qy 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 241 GCTCAAGTGCATCTGCTACTTTCCATGC 270

RESULT 13

US-08-377-687-48
Sequence 48, Application US/08377687
Patent No. 5538525

GENERAL INFORMATION:
APPLICANT: BROEKERT, WILLEM F.
APPLICANT: CAMUE, BRUNO P.A.
APPLICANT: OSBORN, RUPERT W.
APPLICANT: REES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEIDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/377,687
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 414 base pairs

; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..255
US-08-377-687-48

Alignment Scores:

Pred. No.: 1.1e-27 Length: 414
Score: 283.00 Matches: 45
Percent Similarity: 96.00% Conservative: 3
Best Local Similarity: 90.00% Mismatches: 2
Query Match: 92.79% Indels: 0
DB: 1 Gaps: 0

US-10-681-972-2 (1-50) x US-08-377-687-48 (1-414)

Qy 1 ArgLeuCysGluArgProSerGlyThrTyrSerGlyValCysGlyAsnAsnAlaCys 20
Db 106 AAGTTGTGCGAAGGCCCAAGTGGACATGGTCAGAGTCTGTGGAAACATAACGCATGC 165
Qy 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 166 AAGANTCAGTCATTAACCTTGAGAAAGCAGACATGGATCTTGCAACTATGTCTTCCCA 225
Qy 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 226 GCTCACAAGTGTATCTGCTACTTTCTCTGT 255

RESULT 14

US-08-777-192-48
; Sequence 48, Application US/08777192
; Patent No. 5924869

GENERAL INFORMATION:

; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,192
; FILING DATE:
; CLASSIFICATION:

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/002,480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414 base pairs

; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..255
US-08-777-192-48

Alignment Scores:

Pred. No.: 1.1e-27 Length: 414
Score: 283.00 Matches: 45
Percent Similarity: 96.00% Conservative: 3
Best Local Similarity: 90.00% Mismatches: 2
Query Match: 92.79% Indels: 0
DB: 1 Gaps: 0

US-10-681-972-2 (1-50) x US-08-777-192-48 (1-414)

Qy 1 ArgLeuCysGluArgProSerGlyThrTyrSerGlyValCysGlyAsnAsnAlaCys 20
Db 106 AAGTTGTGCGAAGGCCCAAGTGGACATGGTCAGAGTCTGTGGAAACATAACGCATGC 165
Qy 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 166 AAGANTCAGTCATTAACCTTGAGAAAGCAGACATGGATCTTGCAACTATGTCTTCCCA 225
Qy 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 226 GCTCACAAGTGTATCTGCTACTTTCTCTGT 255

RESULT 15

US-08-971-982-48
; Sequence 48, Application US/08971982
; Patent No. 6187904

GENERAL INFORMATION:

; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971,982
; FILING DATE: 17-No. 6187904-1997
; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/002,480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414 base pairs

; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..255
; SEQUENCE DESCRIPTION: SEQ ID NO: 48:
; US-08-971-982-48

Alignment Scores:
Pred. No.: 1.1e-27 Length: 414
Score: 283.00 Matches: 45
Percent Similarity: 96.00% Conservative: 3
Best Local Similarity: 90.00% Mismatches: 2
Query Match: 92.79% Indels: 0
DB: 3 Gaps: 0

US-10-681-972-2 (1-50) x US-08-971-982-48 (1-414)

QY	1	ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys	20
DB	106	AACTTGTGCGAAAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAAACCAATAACGCATGC	165
QY	21	ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro	40
DB	166	AGAATCAGTGCATTAACTTGAAGACGACATGGATCTTGCACACTATGTCTTCCCA	225
QY	41	AlaHisLysCysIleCysTyrPheProCys	50
DB	226	GCTCACAAGGTATCTGCTACTTCTCTTGT	255

Search completed: May 18, 2004, 21:56:21
Job time : 64 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 18, 2004, 21:15:19 ; Search time 289 Seconds
(without alignments)
785.130 Million cell updates/sec

Title: US-10-681-972-2

Perfect score: 305

Sequence: 1 RLCHRPSTGWSGVCNNAC.....EHGSCNVFFPAHKICVYFPC 50

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2947324 seqs, 2269024515 residues

Total number of hits satisfying chosen parameters: 5894648

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA:
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13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2.*
14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
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ALIGNMENTS

RESULT 1

US-09-829-381A-14

; Sequence 14, Application US/09829381A

; Patent No. US20020144306A1

; GENERAL INFORMATION:

; APPLICANT: Liang, Jihong

; Shah, Dilip M.

; Wu, Yonnie S.

; Rosenberger, Cindy A.

; TITLE OF INVENTION: Antifungal Polypeptide and Methods for

; Controlling Plant Pathogenic Fungi

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F

; STREET: 700 Chesterfield Village Parkway No. US20020144306A1th

; CITY: St. Louis

; STATE: Missouri

; COUNTRY: USA

; ZIP: 63198

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

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2	305	100.0	270	13	US-10-681-972-14	Sequence 14, Appl
3	305	100.0	286	9	US-09-829-381A-12	Sequence 12, Appl
4	305	100.0	286	13	US-10-681-972-12	Sequence 12, Appl
5	296	97.0	500	9	US-09-829-381A-9	Sequence 9, Appl
6	296	97.0	500	13	US-10-681-972-9	Sequence 9, Appl
7	283	92.8	285	9	US-09-829-381A-16	Sequence 16, Appl
8	283	92.8	285	13	US-10-681-972-16	Sequence 16, Appl
9	283	92.8	414	9	US-09-759-584-48	Sequence 48, Appl
10	283	92.8	414	13	US-10-388-361A-45	Sequence 45, Appl
11	283	92.8	414	14	US-10-006-252A-19	Sequence 19, Appl
12	278	91.1	403	9	US-09-732-561-13	Sequence 13, Appl
13	274	89.8	285	9	US-09-829-381A-17	Sequence 17, Appl
14	274	89.8	288	13	US-10-681-972-17	Sequence 17, Appl
15	274	89.8	288	9	US-09-759-584-58	Sequence 58, Appl
16	273	89.5	308	9	US-09-829-381A-5	Sequence 5, Appl
17	273	89.5	308	13	US-10-681-972-5	Sequence 5, Appl
18	265	86.9	243	9	US-09-938-842A-2046	Sequence 2046, Ap
19	265	86.9	243	11	US-09-938-842A-2046	Sequence 2046, Ap
20	265	86.9	400	9	US-09-732-561-15	Sequence 15, Appl
21	265	86.9	400	9	US-09-887-576-607	Sequence 607, App
22	265	86.9	1616	9	US-09-732-561-21	Sequence 21, Appl
23	234	76.7	306	9	US-09-829-381A-8	Sequence 8, Appl
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25	196	64.3	284	9	US-09-759-584-50	Sequence 50, Appl
26	175	57.4	373	9	US-09-770-696-283	Sequence 283, App
27	169	55.4	156	15	US-10-178-449A-34	Sequence 34, Appl
28	169	55.4	250	15	US-10-178-449A-36	Sequence 36, Appl
29	169	55.4	610	15	US-10-178-449A-29	Sequence 29, Appl
30	169	55.4	658	15	US-10-178-449A-7	Sequence 7, Appl
31	160	52.5	579	15	US-10-178-449A-31	Sequence 31, Appl
32	157	51.5	150	9	US-09-759-584-31	Sequence 31, Appl
33	157	51.5	529	15	US-10-178-449A-48	Sequence 48, Appl
34	154	50.5	150	9	US-09-759-584-34	Sequence 34, Appl
35	153	50.2	439	15	US-10-178-449A-15	Sequence 15, Appl
36	153	50.2	457	15	US-10-178-449A-13	Sequence 13, Appl
37	153	50.2	458	15	US-10-178-449A-21	Sequence 21, Appl
38	153	50.2	460	15	US-10-178-449A-3	Sequence 3, Appl
39	153	50.2	460	15	US-10-178-449A-17	Sequence 17, Appl
40	153	50.2	461	15	US-10-178-449A-46	Sequence 46, Appl
41	153	50.2	463	15	US-10-178-449A-9	Sequence 9, Appl
42	153	50.2	464	15	US-10-178-449A-19	Sequence 19, Appl
43	153	50.2	472	15	US-10-178-449A-23	Sequence 23, Appl
44	153	50.2	503	15	US-10-178-449A-1	Sequence 1, Appl
45	153	50.2	603	15	US-10-178-449A-11	Sequence 11, Appl

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/829,381A
FILING DATE: 09-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/103,489
FILING DATE: 1998-06-24
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-6224
TELEFAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 270 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-829-381A-14

Alignment Scores:
Pred. No.: 1.27e-33 Length: 270
Score: 305.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-681-972-2 (1-50) x US-09-829-381A-14 (1-270)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 109 AGGTTGTGGAGAGACCAAGTGGACATGTCAGGAGTTTGTGGGAACAACATGCATGC 168
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 169 AGGAACCAATGCAGAAACCTTGAAGAGCAGACACCGATCTTGCAACTATGTCTTCCCA 228

QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 229 GCTCACAATGATTTGTTACTTCCCATGT 258

RESULT 2
US-10-681-972-14
Sequence 14, Application US/10681972
Publication No. US20040064850A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonnie S.
TITLE OF INVENTION: Antifungal Polypeptide AlkVAPP from Alyssum and Methods for Contro
TITLE OF INVENTION: Antifungal Polypeptide AlkVAPP from Alyssum and Methods for Contro
FILE REFERENCE: 38-21 (10700) C
CURRENT APPLICATION NUMBER: US/10/681,972
CURRENT FILING DATE: 2003-10-09
PRIOR APPLICATION NUMBER: US/09/829,381D
PRIOR FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/103,489
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 270
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Plasmid

US-10-681-972-14

Alignment Scores:
Pred. No.: 1.27e-33 Length: 270
Score: 305.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-681-972-2 (1-50) x US-10-681-972-14 (1-270)

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QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 169 AGGAACCAATGCAGAAACCTTGAAGAGCAGACACCGATCTTGCAACTATGTCTTCCCA 228
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 229 GCTCACAATGATTTGTTACTTCCCATGT 258

RESULT 3

US-09-829-381A-12
Sequence 12, Application US/09829381A
Patent No. US20020144306A1

GENERAL INFORMATION:

APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yonnie S.

Rosenberger, Cindy A.

TITLE OF INVENTION: Antifungal Polypeptide and Methods for
Controlling Plant Pathogenic Fungi

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Charles E. Cohen, Monsanto Company, BBAF

STREET: 700 Chesterfield Village Parkway No. US20020144306A1th

CITY: St. Louis

STATE: Missouri

COUNTRY: USA

ZIP: 63198

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/829,381A

FILING DATE: 09-Apr-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/103,489

FILING DATE: 1998-06-24

ATTORNEY/AGENT INFORMATION:

NAME: Cohen, Charles E.

REGISTRATION NUMBER: 34,565

REFERENCE/DOCKET NUMBER: 38-21 (10700)A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (314) 537-6224

TELEFAX: (314) 537-6047

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 286 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-09-829-381A-12

Alignment Scores:

Pred. No.: 1.37e-33 Length: 286
Score: 305.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-681-972-2 (1-50) x US-09-829-381A-12 (1-286)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
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QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
DB 177 AGGAACCAATGCAGAAACCTTGAAGAGAGAGACGATCTTGCAACTATGTCTTCCCA 236

QY 41 AlaHisLysCysIleCysTyrPheProCys 50
DB 237 GCTCACAATGATTTGTTACTTCCCATGT 266

RESULT 4

US-10-681-972-12
; Sequence 12, Application US/10681972
; Publication No. US20040064850A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yennie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alysaum and Methods for Contro
; TITLE OF INVENTION: Antifungal Polypeptide Fungi
; FILE REFERENCE: 38-21 (10700) C
; CURRENT APPLICATION NUMBER: US/10/681,972
; PRIOR FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US/09/829,381D
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/103,489
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 12
; LENGTH: 286
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic PCR reaction product
US-10-681-972-12

Alignment Scores:
Pred. No.: 1.37e-33 Length: 286
Score: 305.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

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QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
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QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
DB 177 AGGAACCAATGCAGAAACCTTGAAGAGAGAGACGATCTTGCAACTATGTCTTCCCA 236

QY 41 AlaHisLysCysIleCysTyrPheProCys 50
DB 237 GCTCACAATGATTTGTTACTTCCCATGT 266

RESULT 5

US-09-829-381A-9

; Sequence 9, Application US/09829381A
; Patent No. US20020144306A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yennie S.
; APPLICANT: Rosenberger, Cindy A.

; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; Controlling Plant Pathogenic Fungi

; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. US20020144306A1th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/829,381A
; FILING DATE: 09-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/103,489
; FILING DATE: 1998-06-24

; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21 (10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 537-6224
; TELEFAX: (314) 537-6047

; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 500 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-829-381A-9

Alignment Scores:
Pred. No.: 5.17e-32 Length: 500
Score: 236.00 Matches: 48
Percent Similarity: 98.00% Conservative: 1
Best Local Similarity: 96.00% Mismatches: 1
Query Match: 97.05% Indels: 0
DB: 9 Gaps: 0

US-10-681-972-2 (1-50) x US-09-829-381A-9 (1-500)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
DB 159 AAGTTGTGCGAGAGTCCAAAGTGGACATGTCAGGCGTGTGGGAATAATAACGCATGC 218

QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
DB 219 AGGAACCAATGCAGAAACCTTGAAGAGAGAGACGATCTTGCAACTATGTCTTCCCA 278

QY 41 AlaHisLysCysIleCysTyrPheProCys 50
DB 279 GCTCACAATGATTTGTTACTTCCCATGT 308

RESULT 6

US-10-681-972-9
; Sequence 9, Application US/10681972
; Publication No. US20040064850A1
; GENERAL INFORMATION:


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1 FILING DATE: 09-Apr-2001
2 CLASSIFICATION: <Unknown>
3 PRIOR APPLICATION DATA:
4 APPLICATION NUMBER: 09/103,489
5 FILING DATE: 1998-06-24
6 ATTORNEY/AGENT INFORMATION:
7 NAME: Cohen, Charles E.
8 REGISTRATION NUMBER: 34,565
9 REFERENCE/DOCKET NUMBER: 38-21 (10700)A
10 TELECOMMUNICATION INFORMATION:
11 TELEPHONE: (314) 537-6224
12 TELEFAX: (314) 537-6047
13 INFORMATION FOR SEQ ID NO: 16:
14 SEQUENCE CHARACTERISTICS:
15 LENGTH: 285 base pairs
16 TYPE: nucleic acid
17 STRANDEDNESS: single
18 TOPOLOGY: linear
19 MOLECULE TYPE: other nucleic acid
20 DESCRIPTION: /desc = "synthetic DNA"
21 SEQUENCE DESCRIPTION: SEQ ID NO: 16:
22 US-09-829-381A-16
23
24 Alignment Scores:
25 Pred. No.: 1,66e-30 Length: 285
26 Score: 283.00 Matches: 45
27 Percent Similarity: 96.00% Conservative: 3
28 Best Local Similarity: 90.00% Mismatches: 2
29 Query Match: 92.79% Indels: 0
30 DB: Gaps: 0
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32 US-10-681-972-2 (1-50) x US-09-829-381A-16 (1-285)
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34 QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
35 Db 121 AAGTTGTGCAGAGGCCATCAGGACTTGTTCAGGAGTCTCGGGAACAACAACGCATGC 180
36
37 QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
38 Db 181 AAGAACCAATGCATCAACCTCGAAGAGCGCATGGATCTTGCACCTACGTCCTCCCA 240
39
40 QY 41 AlaHisLysCysIleCysTyrPheProCys 50
41 Db 241 GCTCACAGTGCATCTGCTACTTTCATGC 270
42
43 RESULT 8
44 US-10-681-972-16
45 Sequence 16, Application US/10681972
46 Publication No. US20040064850A1
47 GENERAL INFORMATION:
48 APPLICANT: Liang, Jihong
49 APPLICANT: Shah, Dilip M.
50 APPLICANT: Wu, Yonnie S.
51 APPLICANT: Rosenberger, Cindy A.
52 TITLE OF INVENTION: Antifungal Polypeptide AUYAPP from Alyssum and Methods for Control
53 TITLE OF INVENTION: Plant Pathogenic Fungi
54 FILE REFERENCE: 38-21 (10700) C
55 CURRENT APPLICATION NUMBER: US/10/681,972
56 CURRENT FILING DATE: 2003-10-09
57 PRIOR APPLICATION NUMBER: US/09/829,381D
58 PRIOR FILING DATE: 2001-04-09
59 PRIOR APPLICATION NUMBER: 09/103,489
60 PRIOR FILING DATE: 1998-06-24
61 NUMBER OF SEQ ID NOS: 20
62 SOFTWARE: Patent in version 3.1
63 SEQ ID NO 16
64 LENGTH: 285
65 TYPE: DNA
66 ORGANISM: Artificial Sequence
67 FEATURE:
68 OTHER INFORMATION: Synthetic
69 US-10-681-972-16

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Alignment Scores: 1.66e-30 Length: 285
Pred. No.: 283.00 Matches: 45
Score: 96.00% Conservative: 3
Percent Similarity: 96.00% Mismatches: 2
Best Local Similarity: 90.00% Indels: 0
Query Match: 92.79% Gaps: 0
DB: 13

US-10-681-972-2 (1-50) x US-10-681-972-16 (1-285)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 121 AAGTTGTGCGAGAGCATCAGGACTTGTCTCAGGAGTCTGTGGAAACAACACGCGATGC 180
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 181 AAGAACCATGCATCAACCTCGAGAGGCACGCGATGATCTTGCACACTACGCTCTCCCA 240
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 241 GCTCACAAGTGCATCTCTACTTTCCTTGT 270

RESULT 9
US-09-759-584-48
; Sequence 48, Application US/09759584
; Patent No. US20010014732A1
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEIDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARB & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/759,584
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/377,687
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..255
US-09-759-584-48

Alignment Scores: 2.69e-30 Length: 414
Pred. No.: 283.00 Matches: 45
Score: 96.00% Conservative: 3
Percent Similarity: 96.00% Mismatches: 2
Best Local Similarity: 90.00% Indels: 0
Query Match: 92.79% Gaps: 0
DB: 9

US-10-681-972-2 (1-50) x US-09-759-584-48 (1-414)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 106 AAGTTGTGCGAAAGCCAAAGTGGACATGCTCAGGAGTCTGTGGAAACAATAACGCGATGC 165
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 166 AAGATCACTGTCATTAACCTTGAGAAAGCAGCATGGATCTTGCACACTATGCTTCCCA 225
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 226 GCTCACAAGTGCATCTCTACTTTCCTTGT 255

RESULT 10
US-10-388-361A-45
; Sequence 45, Application US/10388361A
; Publication No. US20030226169A1
; GENERAL INFORMATION:
; APPLICANT: Van Amerongen, Aart
; APPLICANT: Fant, Franky
; APPLICANT: Borremans, Frans
; APPLICANT: De Samblanx, Geneveva
; APPLICANT: Sitjtsma, Lolke
; APPLICANT: Meloen, Robbert
; APPLICANT: Ruijk, Wouter
; APPLICANT: Schaaper, Wilhelmus
; APPLICANT: Broekaert, Willem
; APPLICANT: Van Gelder, Wilhelms
; APPLICANT: Rees, Sarah
; TITLE OF INVENTION: Antifungal Proteins
; FILE REFERENCE: 50094PPDDIV
; CURRENT APPLICATION NUMBER: US/10/388,361A
; CURRENT FILING DATE: 2003-03-13
; PRIOR APPLICATION NUMBER: US 09/077,948
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: PCT/GB96/03068
; PRIOR FILING DATE: 1996-12-12
; PRIOR APPLICATION NUMBER: GB 9606552.9
; PRIOR FILING DATE: 1996-03-28
; PRIOR APPLICATION NUMBER: GB 9525455.3
; PRIOR FILING DATE: 1995-12-13
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 414
; TYPE: DNA
; ORGANISM: Raphanus sativus
US-10-388-361A-45

Alignment Scores: 2.69e-30 Length: 414
Pred. No.: 283.00 Matches: 45
Score: 96.00% Conservative: 3
Percent Similarity: 96.00% Mismatches: 2
Best Local Similarity: 90.00% Indels: 0
Query Match: 92.79% Gaps: 0
DB: 13

US-10-681-972-2 (1-50) x US-10-388-361A-45 (1-414)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 106 AAGTTGTGCGAAAGCCAAAGTGGACATGCTCAGGAGTCTGTGGAAACAATAACGCGATGC 165
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40

Db 166 AAGAATCAGTGCATTAACCTTGAAGAAGCAGCATGGATCTTGCAACTATGCTTCCCA 225

Qy 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 226 GCTCACAAGTGATCTGCTACTTCTTCTGT 255

RESULT 11

US-10-006-252A-19
; Sequence 19, Application US/10006252A
; Publication No. US20020152498A1
; GENERAL INFORMATION:
; APPLICANT: De Samblanx, Genoveva
; APPLICANT: Broekaert, Willem
; APPLICANT: Rees, Sarah
; TITLE OF INVENTION: Antifungal Proteins
; FILE REFERENCE: SYN-034DV
; CURRENT APPLICATION NUMBER: US/10/006,252A
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 09/077,951
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: GB 9525474.4
; PRIOR FILING DATE: 1995-12-13
; PRIOR APPLICATION NUMBER: PCT/GB96/03065
; PRIOR FILING DATE: 1996-12-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 414
; TYPE: DNA
; ORGANISM: Raphanus sativus
US-10-006-252A-19

Alignment Scores:
Pred. No.: 2,69e-30 Length: 414
Score: 283.00 Matches: 45
Percent Similarity: 96.00% Conservative: 3
Best Local Similarity: 90.00% Mismatches: 2
Query Match: 92.79% Indels: 0
DB: 14 Gaps: 0

US-10-681-972-2 (1-50) x US-10-006-252A-19 (1-414)

Qy 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 106 AAGTTGTGCGAAGAGCCCAAGTGGGACATGTCAGGAGTCTGTGGAACATATACGCAATGC 165
Qy 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 166 AAGAATCAGTGCATTAACCTTGAGAAAGCAGCATGGATCTTGCAACTATGCTTCCCA 225
Qy 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 226 GCTCACAAGTGATCTGCTACTTCTTCTGT 255

RESULT 12

US-09-732-561-13
; Sequence 13, Application US/09732561
; Patent No. US20020035738A1
; GENERAL INFORMATION:
; APPLICANT: Thomma, Bart
; APPLICANT: Terras, Franky
; APPLICANT: Penninckx, Iris
; APPLICANT: Manners, John
; APPLICANT: Kazan, Remal
; APPLICANT: Broekaert, Willem
; TITLE OF INVENTION: Plant Protection Method
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZENECA Ag Products
; STREET: 1800 Concord Pike
; CITY: Wilmington
; STATE: DE

COUNTRY: USA
ZIP: 19850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/732,561
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/202,638
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/01672
FILING DATE: 20-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: PPD 50165/UST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 886-1699
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 403 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
STRAIN: PDF 1.1
US-09-732-561-13

Alignment Scores:
Pred. No.: 1.3e-29 Length: 403
Score: 278.00 Matches: 44
Percent Similarity: 96.00% Conservative: 4
Best Local Similarity: 88.00% Mismatches: 2
Query Match: 91.15% Indels: 0
DB: 9 Gaps: 0

US-10-681-972-2 (1-50) x US-09-732-561-13 (1-403)

Qy 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 116 AAGTTGTGCGAAGAGCCCAAGTGGGACATGTCGAGATTTGCGAAGACAGTAACGCGTGC 175
Qy 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 176 AAGAATCAGTGCATTAACCTTGAGAAAGCAGCATGGATCTTGCAACTATGCTTCCCA 235
Qy 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 236 GCTCACAAGTGATCTGCTACTTCCCATGT 265

RESULT 13

US-09-829-381A-17
; Sequence 17, Application US/09829381A
; Patent No. US20020144306A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; Shah, Dilip M.
; Wu, Yonnie S.
; Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. US20020144306A1ch
; CITY: St. Louis
; STATE: Missouri

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; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/829,381A
; FILING DATE: 09-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/103,489
; FILING DATE: 1998-06-24
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21 (10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 537-6224
; TELEFAX: (314) 537-6047
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 285 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-829-381A-17

Alignment Scores:
Pred. No.: 3.02e-29 Length: 285
Score: 274.00 Matches: 43
Percent Similarity: 94.00% Conservative: 4
Best Local Similarity: 86.00% Mismatches: 3
Query Match: 89.84% Indels: 0
DB: 9 Gaps: 0

US-10-681-972-2 (1-50) x US-09-829-381A-17 (1-285)
QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 121 AAGTTGTGCCAAGGCCATCAGGACTTGGTCAGGAGTCTGCGGAACACACACGCGATGC 180
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 181 AAGAACCACATGCATCAGACTCGAGAAGCGCAGCGCATGGATCTTGCAACTACGCTCTCCCA 240
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 241 GCTCAAGTGCATCTGCTACTTTCCATGC 270

RESULT 14
US-10-681-972-17
; Sequence 17, Application US/10681972
; Publication No. US20040064850A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alysium and Methods for Control
; FILE REFERENCE: 38-21 (10700) C
; CURRENT APPLICATION NUMBER: US/10/681,972
; CURRENT FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US/09/829,381D
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/103,489
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 20

; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/829,381A
; FILING DATE: 09-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/103,489
; FILING DATE: 1998-06-24
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21 (10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 537-6224
; TELEFAX: (314) 537-6047
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 285 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-829-381A-17

Alignment Scores:
Pred. No.: 3.02e-29 Length: 285
Score: 274.00 Matches: 43
Percent Similarity: 94.00% Conservative: 4
Best Local Similarity: 86.00% Mismatches: 3
Query Match: 89.84% Indels: 0
DB: 9 Gaps: 0

US-10-681-972-2 (1-50) x US-09-829-381A-17 (1-285)
QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 121 AAGTTGTGCCAAGGCCATCAGGACTTGGTCAGGAGTCTGCGGAACACACACGCGATGC 180
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 181 AAGAACCACATGCATCAGACTCGAGAAGCGCAGCGCATGGATCTTGCAACTACGCTCTCCCA 240
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 241 GCTCAAGTGCATCTGCTACTTTCCATGC 270

RESULT 15
US-09-759-584-58
; Sequence 58, Application US/09759584
; Patent No. US20010014732A1
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKI R.G.
; APPLICANT: VANDERLEIDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/759,584
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/377,687
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 288 base pairs
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 285
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-681-972-17

Alignment Scores:
Pred. No.: 3.02e-29 Length: 285
Score: 274.00 Matches: 43
Percent Similarity: 94.00% Conservative: 4
Best Local Similarity: 86.00% Mismatches: 3
Query Match: 89.84% Indels: 0
DB: 13 Gaps: 0

US-10-681-972-2 (1-50) x US-10-681-972-17 (1-285)
QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 121 AAGTTGTGCCAAGGCCATCAGGACTTGGTCAGGAGTCTGCGGAACACACACGCGATGC 180
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 181 AAGAACCACATGCATCAGACTCGAGAAGCGCAGCGCATGGATCTTGCAACTACGCTCTCCCA 240
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 241 GCTCAAGTGCATCTGCTACTTTCCATGC 270

RESULT 15
US-09-759-584-58
; Sequence 58, Application US/09759584
; Patent No. US20010014732A1
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKI R.G.
; APPLICANT: VANDERLEIDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/759,584
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/377,687
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 288 base pairs
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; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 43..282
; US-09-759-584-58

Alignment Scores:

Pred. No.:	3.06e-29	Length:	288
Score:	274.00	Matches:	43
Percent Similarity:	94.00%	Conservative:	4
Best Local Similarity:	86.00%	Mismatches:	3
Query Match:	89.84%	Indels:	0
DB:	9	Gaps:	0

US-10-681-972-2 (1-50) x US-09-759-584-58 (1-288)

QY	1	ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys	20
Db	133	AAATTGTGCCAAAGGCCAAGTGGACATGTCAGGAGTCTGTGGAACACATAACGCATGC	192
QY	21	ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro	40
Db	193	AAAGATCAGTGCATTAGACTTGAGAAAGCAGCAGCATGGATCTTGCAACTATGTCCTCCCA	252
QY	41	AlaHisLysCysIleCysTyrPheProCys	50
Db	253	GCTCACAAAGTGATCTGCTACTTCTCTTGT	282

Search completed: May 18, 2004, 22:55:50
Job time : 290 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 18, 2004, 20:22:48 ; Search time 2363 Seconds
(without alignments)
631.870 Million cell updates/sec

Title: US-10-681-972-2

Perfect score: 305

Sequence: 1 RLCERSGTSWGVCGNNAC.....EHGSCNVVFPAAHKICVCFPC 50

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hcc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hcc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vit:*
21: em_gss_fun:*
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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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6	283	92.8	421	14	CD826491	CD826491 BN25.064A
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8	283	92.8	421	14	CD833977	CD833977 BN45.040D
9	283	92.8	422	14	CD833983	CD833983 BN45.040D
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22	283	92.8	803	28	BH458392	BH458392 BOCWE36TF
23	279	91.5	422	14	CD831972	CD831972 BN40.061I
24	278	91.1	318	9	AA713157	AA713157 32717 Lam
25	278	91.1	394	12	BG321454	BG321454 DS01.08H0
26	278	91.1	421	9	AV816118	AV816118 AV816118
27	278	91.1	422	9	AV787956	AV787956 AV787956
28	277	90.8	409	14	CD832294	CD832294 BN40.062L
29	277	90.8	425	14	CD834852	CD834852 BN45.043G
30	277	90.8	427	14	CD833613	CD833613 BN40.067P
31	277	90.8	449	14	CD833047	CD833047 BN40.065M
32	277	90.8	457	14	CD831226	CD831226 BN40.058J
33	277	90.8	473	14	CD834995	CD834995 BN45.043O
34	277	90.8	476	14	CD833784	CD833784 BN45.001I
35	277	90.8	476	14	CD834092	CD834092 BN45.040I
36	277	90.8	481	14	CD833924	CD833924 BN45.040A
37	277	90.8	482	14	CD833627	CD833627 BN45.001A
38	277	90.8	523	14	CD833661	CD833661 BN45.001C
39	277	90.8	543	14	CD828840	CD828840 BN40.040A
40	277	90.8	543	14	CD830628	CD830628 BN40.046D
41	277	90.8	645	14	CD829429	CD829429 BN40.042B
42	277	90.8	762	28	BZ517729	BZ517729 BOMSG66TF
43	274	89.8	421	14	CD837517	CD837517 BN45.052I
44	274	89.8	424	14	CD833048	CD833048 BN40.065M
45	273	89.5	522	14	CD833938	CD833938 BN45.040A

ALIGNMENTS

RESULT 1
CD833779
LOCUS CD833779 408 bp mRNA linear EST 10-JUL-2003
DEFINITION BN45.001115F010914 BN45 Brassica napus cDNA clone BN45001115, mRNA sequence.
ACCESSION CD833779
VERSION CD833779.1 GI:32515719
KEYWORDS EST.
SOURCE Brassica napus (rape)
ORGANISM Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

```

REFERENCE
1 (bases 1 to 408)
Genoplante.
AUTHORS
Genoplante, a major partnership french program in plant genomics
TITLE
Unpublished (2003)
JOURNAL
COMMENT
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com)
and http://genoplante-info.infobiogen.fr.
FEATURES
Location/Qualifiers
1..408
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN4500115"
/tissue_type="seed"
/clone_lib="BN45"
ORIGIN
Alignment Scores:
Pred. No.: 7.23e-22 Length: 408
Score: 283.00 Matches: 45
Percent Similarity: 96.00% Conservative: 3
Best Local Similarity: 90.00% Mismatches: 2
Query Match: 92.79% Indels: 0
DB: 14 Gaps: 0
US-10-681-972-2 (1-50) x CD833779 (1-408)
QY 1 ArgLeuCysGluArgProSerGlyThrTpsSerGlyValCysGlyAsnAsnAlaCys 20
Db 118 AGTTGTGGAGAGGCCAAGTGGACATGCTCAGGAGCTCGCGAAGCAATACGCATGC 177
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 178 AAGATCAGTGCATTAACTTGAAGAACGACGACATGATCTTGCACATATGCTTCCCA 237
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 238 GCTCACAAGTATTGCTACTTCCCTTGT 267
RESULT 2
CD834090 409 bp mRNA linear EST 10-JUL-2003
LOCUS
DEFINITION
BN45.040121F011018 BN45 Brassica napus cDNA clone BN45040121, mRNA
sequence.
ACCESSION
CD834090
VERSION
CD834090.1 GI:32516030
KEYWORDS
Brassica napus (rape)
SOURCE
Brassica napus
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 409)
AUTHORS
Genoplante.
TITLE
Unpublished (2003)
JOURNAL
COMMENT
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com)
and http://genoplante-info.infobiogen.fr.
FEATURES
Location/Qualifiers
1..409
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN4500115"
/tissue_type="seed"
/clone_lib="BN45"
ORIGIN
Alignment Scores:
Pred. No.: 7.48e-22 Length: 418
Score: 283.00 Matches: 45
Percent Similarity: 96.00% Conservative: 3
Best Local Similarity: 90.00% Mismatches: 2
Query Match: 92.79% Indels: 0
DB: 14 Gaps: 0
US-10-681-972-2 (1-50) x CD834090 (1-409)
QY 1 ArgLeuCysGluArgProSerGlyThrTpsSerGlyValCysGlyAsnAsnAlaCys 20
Db 119 AGTTGTGGAGAGGCCAAGTGGACATGCTCAGGAGCTCGCGAAGCAATACGCATGC 178
QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db 179 AAGATCAGTGCATTAACTTGAAGAACGACGACATGATCTTGCACATATGCTTCCCA 238
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 239 GCTCACAAGTATTGCTACTTCCCTTGT 268
RESULT 3
CD832625 418 bp mRNA linear EST 10-JUL-2003
LOCUS
DEFINITION
BN40.064A14F011227 BN40 Brassica napus cDNA clone BN40064A14, mRNA
sequence.
ACCESSION
CD832625
VERSION
CD832625.1 GI:32514565
KEYWORDS
Brassica napus (rape)
SOURCE
Brassica napus
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 418)
AUTHORS
Genoplante.
TITLE
Unpublished (2003)
JOURNAL
COMMENT
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com)
and http://genoplante-info.infobiogen.fr.
FEATURES
Location/Qualifiers
1..418
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN40064A14"
/tissue_type="seed"
/clone_lib="BN40"
ORIGIN
Alignment Scores:
Pred. No.: 7.48e-22 Length: 418
Score: 283.00 Matches: 45
Percent Similarity: 96.00% Conservative: 3
Best Local Similarity: 90.00% Mismatches: 2
Query Match: 92.79% Indels: 0
DB: 14 Gaps: 0

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US-10-681-972-2 (1-50) x CD832625 (1-418)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
 Db 143 AAGTTGTGCGAGAGGCCAAGTGGACATGTCAGGAGTCTGTGGAACAATAACGCATGC 202
 QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
 Db 203 AAGATCAGTGCATTACCTTGTGGAAGACGACATGATCTTGCACATATGCTTCCCA 262
 QY 41 AlaHisLysCysIleCysTyrPheProCys 50
 Db 263 GCTCACAAAGTGATTGCTACTTCCCTTGT 292

RESULT 4

CD834168
 LOCUS BN45.040N06F011018 BN45 Brassica napus cDNA clone BN45040N06, mRNA
 DEFINITION sequence.

ACCESSION CD834168

VERSION CD834168.1 GI:32516108

KEYWORDS EST.

SOURCE Brassica napus (rape)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 419)

AUTHORS

TITLE

JOURNAL

COMMENT

Genoplatte

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french

plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>

and <http://genoplatte-info.infobiogen.fr>).

FEATURES

source

1..419
 /organism="Brassica napus"
 /mol_type="mRNA"
 /cultivar="Jet neuf"
 /db_xref="taxon:3708"
 /clone="BN45040N06"
 /tissue_type="seed"
 /clone_lib="BN45"

ORIGIN

Alignment Scores:
 Pred. No.: 7,51e-22 Length: 419
 Score: 283.00 Matches: 45
 Percent Similarity: 96.00% Conservative: 3
 Best Local Similarity: 90.00% Mismatches: 2
 Query Match: 92.79% Indels: 0
 DB: 14 Gaps: 0

US-10-681-972-2 (1-50) x CD834168 (1-419)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
 Db 140 AAGTTGTGCGAGAGGCCAAGTGGACATGTCAGGAGTCTGTGGAACAATAACGCATGC 199
 QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
 Db 200 AAGATCAGTGCATTACCTTGTGGAAGACGACATGATCTTGCACATATGCTTCCCA 259
 QY 41 AlaHisLysCysIleCysTyrPheProCys 50
 Db 260 GCTCACAAAGTGATTGCTACTTCCCTTGT 289

RESULT 5

CD833944

LOCUS

DEFINITION

sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Brassica napus (rape)

Brassica napus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 420)

AUTHORS

TITLE

JOURNAL

COMMENT

Genoplatte

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french

plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>

and <http://genoplatte-info.infobiogen.fr>).

FEATURES

source

1..420
 /organism="Brassica napus"
 /mol_type="mRNA"
 /cultivar="Jet neuf"
 /db_xref="taxon:3708"
 /clone="BN45040B07"
 /tissue_type="seed"
 /clone_lib="BN45"

ORIGIN

Alignment Scores:
 Pred. No.: 7,53e-22 Length: 420
 Score: 283.00 Matches: 45
 Percent Similarity: 96.00% Conservative: 3
 Best Local Similarity: 90.00% Mismatches: 2
 Query Match: 92.79% Indels: 0
 DB: 14 Gaps: 0

US-10-681-972-2 (1-50) x CD833944 (1-420)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
 Db 140 AAGTTGTGCGAGAGGCCAAGTGGACATGTCAGGAGTCTGTGGAACAATAACGCATGC 199
 QY 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
 Db 200 AAGATCAGTGCATTACCTTGTGGAAGACGACATGATCTTGCACATATGCTTCCCA 259
 QY 41 AlaHisLysCysIleCysTyrPheProCys 50
 Db 260 GCTCACAAAGTGATTGCTACTTCCCTTGT 289

RESULT 6

CD826491

LOCUS

DEFINITION

sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Brassica napus (rape)

Brassica napus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 421)

AUTHORS

Genoplatte.

CD833944
 LOCUS BN45.040B07F011019 BN45 Brassica napus cDNA clone BN45040B07, mRNA
 DEFINITION sequence.

ACCESSION CD833944

VERSION CD833944.1 GI:32515884

KEYWORDS EST.

SOURCE Brassica napus (rape)

Brassica napus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 420)

AUTHORS

TITLE

JOURNAL

COMMENT

Genoplatte

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french

plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>

and <http://genoplatte-info.infobiogen.fr>).

FEATURES

source

1..420

/organism="Brassica napus"

/mol_type="mRNA"

/cultivar="Jet neuf"

/db_xref="taxon:3708"

/clone="BN45040B07"

/tissue_type="seed"

/clone_lib="BN45"

This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (<http://www.genoplante.com>) and <http://genoplante-info.infobiogen.fr>).

Best Local Similarity:	90.00%
Query Match:	92.79%
DB:	14
Mis	
Ind	
Gap	

201 AAGAATCAGTCGATTAACCTTGA AAAAGCAGCATGATCTTGCACATATGCTTCCCA 260

CD833977	CD833977	421 bp	linear	EST 10-JUL-2003		
LOCUS	BN45.040D05F011019	BN45	Brassica napus	cdna clone BN4504D05, mRNA		
DEFINITION	sequence.					
ACCESSION	CD833977					
VERSION	CD833977.1	GI:32515917				
KEYWORDS	EST.					
SOURCE	Brassica napus (rape)					
ORGANISM	Brassica napus					
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.					
	1 (bases 1 to 421)					

COMMENT

Contact: Genoplatante
Genoplatante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplatante' (<http://www.genoplatante.com>
and <http://genoplatante-info.infobiogen.fr>).

```

/db_xref="taxon:3708"
/clone="BN45040D05"
/tissue_type="seed"
/clone_lib="BN45"

```

Alignment Scores:	
Pred. No.:	7,566-22
Score:	283.00
Percent Similarity:	96.00%
Best local Similarity:	90.00%
Query Match:	92.79%
DR.	14
	Can
	ind
	Mis
	Con
	Mat
	Len

US-10-6A1-972-2 (1-50) x CD8333977 (1-421)
 Query Match: 52.75%
 DB: 14 Gap

```

QY      1  ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
141    AAGTTGTGCGAGAGGCCAAGTGGACATGGTCAGAGTCTGTGGAAACAATAACGCATGC 200
QY      21  ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
201    AAGAATCAGTGCATTAACCTTGAGAAAGCAGACATGGATCTTGCAACTATGTCTTCCCA 260

QY      41  AlahisLysCysIleCysTyrPheProCys 50
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
261    GCTCACAGTGTATTGTCTACTTCCCTTGT 290

RESULT 9
CD833983
LOCUS      CD833983               422 bp    mRNA    linear    EST 10-JUL-2003
DEFINITION BN45.040D11F011019 BN45 Brassica napus cDNA clone BN45040D11, mRNA
sequence.
ACCESSION CD833983
VERSION    CD833983.1 GI:32515923
KEYWORDS   EST.
SOURCE     Brassica napus (rape)
ORGANISM   Brassica napus
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
           rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 422)
AUTHORS   Genoplatne, a major partnership french program in plant genomics
TITLE     Genoplatne, a major partnership french program in plant genomics
JOURNAL   Unpublished (2003)
COMMENT   Contact: Genoplatne
           Genoplatne
           93, rue Henri Rochefort 91025 EVRY CEDEX France
           Tel: 33 1 69 47 54 00
           Fax: 33 1 69 47 54 10
           This sequence has been generated in the framework of the french
           plant genomics programme 'Genoplatne' (http://www.genoplatne.com)
           and http://genoplatne-info.infobiogen.fr.

FEATURES             source
     source           1..422
                     /organism="Brassica napus"
                     /mol_type="mRNA"
                     /cultivar="Jet neuf"
                     /db_xref="taxon:3708"
                     /clone="BN45040D11"
                     /tissue_type="seed"
                     /clone_lib="BN45"

ORIGIN
Alignment Scores:
Pred. No.:          7.59e-22          Length:          422
Score:              283.00           Matches:         45
Percent Similarity: 96.00%           Conservative:    3
Best Local Similarity: 90.00%         Mismatches:     2
Query Match:        92.79%           Indels:         0
DB:                 14              Gaps:           0

US-10-681-972-2 (1-50) x CD833983 (1-422)

QY      1  ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
141    AAGTTGTGCGAGAGGCCAAGTGGACATGGTCAGAGTCTGTGGAAACAATAACGCATGC 200
QY      21  ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
201    AAGAATCAGTGCATTAACCTTGAGAAAGCAGACATGGATCTTGCAACTATGTCTTCCCA 260

QY      41  AlahisLysCysIleCysTyrPheProCys 50
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
261    GCTCACAGTGTATTGTCTACTTCCCTTGT 290

RESULT 10
CD827413
LOCUS      CD827413               426 bp    mRNA    linear    EST 10-JUL-2003
DEFINITION BN25.067G02F020123 BN25 Brassica napus cDNA clone BN25067G02, mRNA
sequence.
ACCESSION CD827413
VERSION    CD827413.1 GI:32509353
KEYWORDS   EST.
SOURCE     Brassica napus (rape)
ORGANISM   Brassica napus
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
           rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 426)
AUTHORS   Genoplatne, a major partnership french program in plant genomics
TITLE     Genoplatne, a major partnership french program in plant genomics
JOURNAL   Unpublished (2003)
COMMENT   Contact: Genoplatne
           Genoplatne
           93, rue Henri Rochefort 91025 EVRY CEDEX France
           Tel: 33 1 69 47 54 00
           Fax: 33 1 69 47 54 10
           This sequence has been generated in the framework of the french
           plant genomics programme 'Genoplatne' (http://www.genoplatne.com)
           and http://genoplatne-info.infobiogen.fr.

FEATURES             source
     source           1..426
                     /organism="Brassica napus"
                     /mol_type="mRNA"
                     /cultivar="Jet neuf"
                     /db_xref="taxon:3708"
                     /clone="BN25067G02"
                     /tissue_type="seed"
                     /clone_lib="BN25"

ORIGIN
Alignment Scores:
Pred. No.:          7.69e-22          Length:          426
Score:              283.00           Matches:         45
Percent Similarity: 96.00%           Conservative:    3
Best Local Similarity: 90.00%         Mismatches:     2
Query Match:        92.79%           Indels:         0
DB:                 14              Gaps:           0

US-10-681-972-2 (1-50) x CD827413 (1-426)

QY      1  ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
141    AAGTTGTGCGAGAGGCCAAGTGGACATGGTCAGAGTCTGTGGAAACAATAACGCATGC 200
QY      21  ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
201    AAGAATCAGTGCATTAACCTTGAGAAAGCAGACATGGATCTTGCAACTATGTCTTCCCA 260

QY      41  AlahisLysCysIleCysTyrPheProCys 50
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
261    GCTCACAGTGTATTGTCTACTTCCCTTGT 290

RESULT 11
CD831294
LOCUS      CD831294               438 bp    mRNA    linear    EST 10-JUL-2003
DEFINITION BN40.058N13F011019 BN40 Brassica napus cDNA clone BN40058N13, mRNA
sequence.
ACCESSION CD831294
VERSION    CD831294.1 GI:32513234
KEYWORDS   EST.
SOURCE     Brassica napus (rape)
ORGANISM   Brassica napus
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
           rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 438)
AUTHORS   Genoplatne, a major partnership french program in plant genomics
TITLE     Genoplatne, a major partnership french program in plant genomics
JOURNAL   Unpublished (2003)

```

COMMENT

Contact: Genoplatte
Genoplatte
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>
and <http://genoplatte-info.infobiogen.fr>).

FEATURES

source
1..438
Location/Qualifiers
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN40059J13"
/tissue_type="seed"
/clone_lib="BN40"

ORIGIN

Alignment Scores:
Pred. No.: 7,99e-22 Length: 438
Score: 283.00 Matches: 45
Percent Similarity: 96.00% Conservative: 3
Best Local Similarity: 90.00% Mismatches: 2
Query Match: 92.79% Indels: 0
DB: 14 Gaps: 0

US-10-681-972-2 (1-50) x CD831294 (1-438)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
:::|||||
DB 141 AAGTTGCGAAGGCCAAGTGGACATGTCAGGAGTCTGTGGAAACAATAACGATGC 200
21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
:::|||||
DB 201 AAGATCAGTCATTAACCTTGAGAAAGCAGACATGATCTTGCAACTATGCTTCCCA 260
41 AlaHisLysCysIleCysTyrPheProCys 50
:::|||||
DB 261 GCTCACAAGTGATTTGCTACTTCCCTTGT 290

RESULT 12

CD831479
LOCUS
DEFINITION
CD831479 438 bp mRNA linear EST 10-JUL-2003
BN40.059J13F011208 BN40 Brassica napus cDNA clone BN40059J13, mRNA
sequence.

ACCESSION
CD831479

VERSION
CD831479.1 GI:32513419

KEYWORDS
EST.

SOURCE
Brassica napus (rape)

ORGANISM

Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 438)

Genoplatte.

Genoplatte, a major partnership french program in plant genomics

Unpublished (2003)

Contact: Genoplatte

Genoplatte

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french
plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>
and <http://genoplatte-info.infobiogen.fr>).

FEATURES

source
1..438
Location/Qualifiers
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN40059J13"

ORIGIN

Alignment Scores:

Pred. No.: 7,99e-22 Length: 438
Score: 283.00 Matches: 45
Percent Similarity: 96.00% Conservative: 3
Best Local Similarity: 90.00% Mismatches: 2
Query Match: 92.79% Indels: 0
DB: 14 Gaps: 0

US-10-681-972-2 (1-50) x CD831479 (1-438)

QY 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
:::|||||
DB 141 AAGTTGCGAAGGCCAAGTGGACATGTCAGGAGTCTGTGGAAACAATAACGATGC 200
21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
:::|||||
DB 201 AAGATCAGTCATTAACCTTGAGAAAGCAGACATGATCTTGCAACTATGCTTCCCA 260
41 AlaHisLysCysIleCysTyrPheProCys 50
:::|||||
DB 261 GCTCACAAGTGATTTGCTACTTCCCTTGT 290

RESULT 13

CD834068
LOCUS
DEFINITION
CD834068 446 bp mRNA linear EST 10-JUL-2003
BN45.040H17F011019 BN45 Brassica napus cDNA clone BN45040H17, mRNA
sequence.

ACCESSION
CD834068

VERSION
CD834068.1 GI:32516008

KEYWORDS
EST.

SOURCE
Brassica napus (rape)

ORGANISM

Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 446)

Genoplatte.

Genoplatte, a major partnership french program in plant genomics

Unpublished (2003)

Contact: Genoplatte

Genoplatte

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french
plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>
and <http://genoplatte-info.infobiogen.fr>).

FEATURES

source
1..446
Location/Qualifiers
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN45040H17"
/tissue_type="seed"
/clone_lib="BN45"

ORIGIN

Alignment Scores:

Pred. No.: 8,19e-22 Length: 446
Score: 289.00 Matches: 45
Percent Similarity: 96.00% Conservative: 3
Best Local Similarity: 90.00% Mismatches: 2
Query Match: 92.79% Indels: 0
DB: 14 Gaps: 0

US-10-681-972-2 (1-50) x CD834068 (1-446)

QY

1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20

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Db      156 AAGTTGTGGAGAGCCAGTGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC 215
QY      21  ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db      216 AAGAATCATGTCATTAACTTGGAGAAAGCAGACATGGATCTTGCAACTATGTCTTCCCA 275
QY      41  AlaHisLysCysIleCysTyrPheProCys 50
Db      276 GCTCAAGTGTATTGTCTACTTCCCTTGT 305

RESULT 14
LOCUS   CD832592
DEFINITION BN40.063015F011228 BN40 Brassica napus cDNA clone BN40063015, mRNA
sequence.
ACCESSION CD832592
VERSION   CD832592.1
KEYWORDS EST.
SOURCE    Brassica napus (rape)
ORGANISM  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 447)
AUTHORS   Genoplante.
TITLE     Genoplante, a major partnership french program in plant genomics
JOURNAL   Unpublished (2003)
COMMENT   Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
FEATURES
source
1..447
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN40063015"
/tissue_type="seed"
/clone_lib="BN40"
ORIGIN
Alignment Scores:
Pred. No.: 8,22e-22 Length: 447
Score: 283.00 Matches: 45
Percent Similarity: 96.00% Conservative: 3
Best Local Similarity: 90.00% Mismatches: 2
Query Match: 92.79% Indels: 0
DB: 14 Gaps: 0
US-10-681-972-2 (1-50) x CD832592 (1-447)
QY      1  ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db      155 AAGTTGTGGAGAGGCCAAGTGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC 214
QY      21  ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db      215 AAGAATCATGTCATTAACTTGGAGAAAGCAGACATGGATCTTGCAACTATGTCTTCCCA 274
QY      41  AlaHisLysCysIleCysTyrPheProCys 50
Db      275 GCTCAAGTGTATTGTCTACTTCCCTTGT 304

RESULT 15
LOCUS   CD834611
DEFINITION BN45.042H07F011228 BN45 Brassica napus cDNA clone BN45042H07, mRNA
sequence.
ACCESSION CD834611
VERSION   CD834611.1
KEYWORDS EST.
SOURCE    Brassica napus (rape)
ORGANISM  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 450)
AUTHORS   Genoplante.
TITLE     Genoplante, a major partnership french program in plant genomics
JOURNAL   Unpublished (2003)
COMMENT   Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
FEATURES
source
1..450
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN45042H07"
/tissue_type="seed"
/clone_lib="BN45"
ORIGIN
Alignment Scores:
Pred. No.: 8,3e-22 Length: 450
Score: 283.00 Matches: 45
Percent Similarity: 96.00% Conservative: 3
Best Local Similarity: 90.00% Mismatches: 2
Query Match: 92.79% Indels: 0
DB: 14 Gaps: 0
US-10-681-972-2 (1-50) x CD834611 (1-450)
QY      1  ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db      156 AAGTTGTGGAGAGGCCAAGTGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGT 215
QY      21  ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
Db      216 AAGAATCATGTCATTAACTTGGAGAAAGCAGACATGGATCTTGCAACTATGTCTTCCCA 275
QY      41  AlaHisLysCysIleCysTyrPheProCys 50
Db      276 GCTCAAGTGTATTGTCTACTTCCCTTGT 305

Search completed: May 18, 2004, 21:54:56
Job time : 2364 secs

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